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May 9, 2006, 01:18:21; Search time 106.251 Seconds (without alignments) 487.964 Million cell updates/sec
                                                                                                                                                                                                      118
                                                                                                                                                                  US-10-700-632-7
622
1 QVQLQQPGAEVVKPGASVKM......EVRLRYFDVWGAGTTVTVSS
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                             2443163
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            2443163 segs, 439378781 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2004s:*
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Perfect
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:\*

	Description	Ado32091 Mouse ant	Ado32157 Mouse ant	Ado32093 Humanised	Adj94605 Chimeric	Adj94607 Chimeric	Aar55215 Murine va	Aab30694 A fusion	Abj39009 B9E9 scFv	Abr55873 Anti-CD20	Abu08394 Murine an	Adc66270 Mouse ant	Ade85690 Murine im	Ade73084 Murine FU	Adf60661 Protein r	Adn49734 Mature va	Adu74410 Mouse ant	Adv92492 2B8 heavy	Adv98555 Novel chi	Adz59909 Glycoprot	_	Abb82833 Antibody	Adw77074 Heavy cha	Ad192472 Antibody	Ad192473 Improved
SUMMARIES	Ü	ADO32091	AD032157	AD032093	ADJ94605	ADJ94607	AAR55215	AAB30694	ABJ39009	ABR55873	ABU08394	ADC66270	ADE85690	ADE73084	ADF60661	ADN49734	ADU74410	ADV92492	ADV98555	ADZ59909	AAE27924	ABB82833	ADW77074	ADL92472	ADL92473
	Length DB	118 8	117 8	118 8	121 7	121 7	140 2	412 4	412 6	140 6	140 6	140 7	140 7	140 7	140 7	140 8	140 8	•	140 9	-	360 5	360 6	368 9	451 8	451 8
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	& Query Match	100.0	99.4	98.6	86.3	86.	82	85	85	85	82	85	85	85	85.	85.	82	85	85.	85	85.	85.	85.	82	82
	Score	622	618	613	536.5	536.5	534.5	534.5	534.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5	533.5
	Result No.	П	8	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

Adu68155 Novel var Adu68154 Novel var Aab08026 A dimeric Aae27923 Human C28		Adv98563 Novel chi Adv92502 CD20VH/FC Adv98565 Novel chi Adv92504 FL/FC/CD2		Aac27201 Murine an AAX16286 2BB antib AdV21492 Human ant AAX16294 Luel6 ant Adz83548 CD20 VH.
3 ADU68155 3 ADU68154 5 AAB08026 5 AAE27923	ABB82832 ADV92496 ADV98559 ADV92500	ADV98563 ADV92502 ADV98565 ADV92504	<ul><li>ADV98567</li><li>ADJ94601</li><li>AAB30695</li><li>ABJ39010</li></ul>	AAO27201 ADX16286 ADV21492 ADX16294 ADX83548
451 451 470 470	470 470 626	626 641 641 657	657 120 423 423	12221122
3.5 85.8 3.5 85.8 3.5 85.8	3.5 85.8 3.5 85.8 3.5 85.8	8.55 8.55 8.55 8.56 8.56 8.56 8.56	8.5 85.5 0.5 85.3 0.5 85.3	527 84.7 6.5 84.6 521 83.8 521 83.8 521 83.8
25 533 26 533 27 533 28 533	29 533.5 30 533.5 31 533.5 32 533.5	334 533 34 533 35 533 36 533	37 533.5 38 531.5 39 530.5 40 530.5	41 422 526 44 45 45 522 522 522 522 522 523

## ALIGNMENTS

AD032091 standard; protein; 118 AA

RESULT 1 ADO32091

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New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute or chronic myeloid leukemia.
                                                            Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.
                                                                                  anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 7; 124pp; English.
                                                                                                                                                                                                                                                                                       Lutz RJ;
                                                                                                                                                                                                                       05-NOV-2003; 2003WO-US032737.
                                                                                                                                                                                                                                           07-NOV-2002; 2002US-0424332P.
                                          (first entry)
                                                                                                                                                                                                                                                                                      Hoffee MG, Tavares D,
                                                                                                                                                                                                                                                                 (IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                            WPI; 2004-411619/38.
                                                                                                                                                                                                                                                                                                                       N-PSDB; AD032140.
                                                                                                                                                                            WO2004043344-A2.
                                                                                                                                                      Mus musculus
                                         12-AUG-2004
                                                                                                                                                                                                  27-MAY-2004.
                                                                                                                                   heavy chain.
                     AD032091;
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defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or its epitope-binding fragment, immunoconjugate, or defined antibody or its epitope-binding fragment, immunoconjugate, or defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment celling a nisolated polymucleotide encoding the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polymucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) obtaining CD33 from a biological material. The anti-CD33 antibody has cycostation can be used for trasting a subject having a disease where CD3 is expressed, such as myelodyaplastic syndrome, acute composition can be used for trasting a subject having a disease where CD3 is expressed, such as myelodyaplastic syndrome, and for an averaging or anti-CD33 antibody My9-6 heavy chain conjugate, and for in vivo imaging or as affinity purification agents. The present variable region, which is used in an example from the present invention. composition comprising the immunoconjugate, composition or the antibody 8888888888888888888888888888888

Sequence 118 AA;

9 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118 61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY Gape .. 0 Length 118; Indels ö 100.0%; Score 622; DB 8; 100.0%; Pred. No. 2.6e-45; 0; Mismatches Query Match
Best Local Similarity 100.
Matches 118; Conservative 요 ð ò

12-AUG-2004 AD032157; RESULT 2 ADO32157

ADO32157 standard; protein; 117 AA. (first entry)

anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain. Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73. 

Mus musculus.

WO2004043344-A2.

27-MAY-2004

05-NOV-2003; 2003WO-US032737.

07-NOV-2002; 2002US-0424332P.

(IMMU-) IMMUNOGEN INC.

Lutz RJ; Tavares D, Hoffee MG,

WPI; 2004-411619/38.

New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute

The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity—determining region (CDR), or (b) at least heavy chain variable region. GDR, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunocollygate comprising the antibody or its epitope-binding fragment and a drug or prodrug; (2) a composition comprising the antibody or prodrug in comprising the antibody or prodrug in a pharmaceutical composition comprising the immunocollygate, composition of the antibody or attibody fragment is labelled; (5) inhibiting the where the antibody or antibody fragment is labelled; (5) inhibiting the approach of antibody or attibody fragment is labelled; (5) inhibiting the where the antibody or attibody fragment is labelled; (5) inhibiting the contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment, immunoconjugate, or contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD3; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment (10) are recombinant vector comprising the polynucleotide, (11) a host cell cransformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) cobtaining fragment that specifically binds to bind CD33; and (13) cobtaining fragment having the ability to bind CD33; and (13) cobtaining fragment having the ability to bind cD33; and coptaining fragment coptaining fragment having the ability to bind cD33; and coptaining fragment having the ability to bind cD33; and coptaining fragment having the sused for transiting a subject having a immunoconjugate, composition can be used for transiting a subject having a coptaining fragment can be used for the present or in vivo imaging or as affinity purification agents. The present continued and an expense or an expense or an Example 3; SEQ ID NO 73; 124pp; English. or chronic myeloid leukemia. Sequence 117 AA; invention. 

Gaps . 0 0; Indels 99.4%; Score 618; DB 8; I 100.0%; Pred. No. 5.6e-45; iive 0; Mismatches 0; Matches 117; Conservative Local Similarity Query Match

QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60 9 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY

ઠ 셤 ઠે 셤

61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVS 117 NOKFKGKATLITADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVS 117

RESULT 3

ADO32093;

ADO32093 standard; protein; 118 AA

12-AUG-2004 (first entry)

Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.

anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6; heavy chain.

Mus musculus. 

Homo sapiens. Synthetic.

(first entry)

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New humanized anti-CD20 monoclonal antibody (MAb) that retains ubstrantially the B-cell and B-cell lymphoma and leukemia cell targeting of the murine anti-CD20 MAb, useful for treating B-cell lymphoma, leukemia or an autoimmune diseases.
                                                                                                                                                numanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
                                                                                                                                                                          IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease; thrombocytopenia; lupus; rheumatoid arthritis;
                                                                                                  Chimeric anti-CD20 antibody variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qu Z, Goldenberg DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2002; 2002US-0356132P. 07-OCT-2002; 2002US-0416232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2003; 2003WO-GB000665
                                                                                                                                                                                                                      neavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMUNOMEDICS INC (MCCA/) MCCALL J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-697522/66.
N-PSDB; ADJ94604.
                                                                                                                                                                                                                                                                                                                                                     WO2003068821-A2.
                                                                                                                                                                                                                                                                                                 Unidentified.
                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hansen H,
  ADJ94605;
                                                                                                                                                                                                                                                                               Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated anni-tube antipody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or is producing; (2) a composition comprising the antibody or producing (3) a pharmaceutical composition comprising the immunoconjugate, composition or the natibody or antibody or antibody fragment is labelled; (3) inhibiting the defined above, or its epitope-binding fragment; (4) a diagnostic reagen comprising the antibody of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment; (1) immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (6) it (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment; (10) carecombinant vector comprising the polymucleotide encoding a light or heavy care comprising the polymucleotide encoding a light or heavy contains of the antibody defined above or its epitope-binding fragment; (10) are secondinant vector comprising the polymucleotide encoding a subject having a creme with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) cotaining CD33 from a biological material. The antibody we rette encompant or activity. The antibody or its epitope-binding antibody or its epitope-binding fragment having the ability to bind CD33; and (13) expressed, such as myelody place comprising to a subject having a cutivity. The antibody or its epitope-binding and encounted for in vivo imaging or as affinity purification agents. The present contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute or chronic myeloid leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes an isolated anti-CD33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 613; DB 8;
Pred. No. 1.5e-44;
1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 9; 124pp; English.
                                                                                                                                                                                                                                                   Lutz RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%;
98.3%;
                                                                                                  05-NOV-2003; 2003WO-US032737.
                                                                                                                                                07-NOV-2002; 2002US-0424332P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.3
Matches 116; Conservative
                                                                                                                                                                                                                                                   Tavares D,
                                                                                                                                                                                                  (IMMU-) IMMUNOGEN INC
                                                                                                                                                                                                                                                                                                 WPI; 2004-411619/38.
WO2004043344-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 118 AA;
                                                 27-MAY-2004
                                                                                                                                                                                                                                                   Hoffee MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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61 NOKFKGKATLITADKSSTTAYMOLSSLITSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NQKFKGKATLITADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFDVWGQGTTVTVS 120
                                                                                         (MAb) or its antigen-binding fragment containing the complementarity determining regions (CDRs) of at least one murine anti-CD20 Mab variable region and the framework regions (FRs) of at least one human IV1AB variable region. The antibodies of the invention are useful for diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The present amino acid sequence represents a chimeric anti-CD20 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                           invention comprises a humanised anti-CD20 (hCD20)monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                               86.3%; Score 536.5; DB 7; Length 121; 84.3%; Pred. No. 5e-38; ive 6; Mismatches 10; Indels 3.
Disclosure; Fig 2B; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ94607 standard; protein; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                           variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121 AA;
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ID ADJ9
XX
AC ADJ9
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ADJ94605 standard; protein; 121 AA.

ADJ94605 ID ADJ9 XX RESULT

ò d ਨੇ 셤

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Murine variable region heavy chain from 2BS
                                                                                                                                                                                                                          WPI; 1994-183162/22
                                                                                                                                                                                                                                       N-PSDB; AAQ65631.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptavidin;
hematological
                                                                                                                                                                                          Anderson DR,
                                                    Mus musculus
                                                                        WO9411026-A2
                                                                                                                  12-NOV-1993;
                                                                                                                                      13-NOV-1992;
03-NOV-1993;
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                                                                                              26-MAY-1994
                                                                                                                                                                                                                                                                               hybridomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB30694;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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Protein
                                                                                                                                                                                                     Reff ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
LHXSSSXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFDVWGQGTTVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                   New humanized anti-CD20 monoclonal antibody (MAb) that retains substantially the B-cell and B-cell lymphoma and leukemia cell targeting of the murine anti-CD20 MAb, useful for treating B-cell lymphoma, leukemia or an autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                       (MAb) or its antigen-binding fragment containing the complementarity determining regions (CDRs) of at least one murine anti-CD20 Mab variable region and the framework regions (FRs) of at least one human IVIAB variable region. The antibodies of the invention are useful for diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune disease (e.g. thrombocytopenia, lupus or rheumatoid archiritis). The present amino acid sequence represents a chimeric anti-CD20 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb; IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease; thrombocytopenia; lupus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                              invention comprises a humanised anti-CD20 (hCD20)monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQQPGAEVVKPGASVKMSCKASGYTPTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                     Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 536.5; DB 7;
Pred. No. 5e-38;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR55215
ID AAR55215 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                         Claim 22; Fig 4A; 106pp; English.
                                                                                                                                                                                                                                                          Goldenberg DM;
                                                                                                                                                                       14-FEB-2003; 2003WO-GB000665
                                                                                                                                                                                                     07-OCT-2002; 2002US-0416232P
                                                                                                                                                                                            14-FEB-2002; 2002US-0356132P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.3%;
84.3%;
                                                                        heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                                                           (IMMI-) IMMINOMEDICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variable heavy chain.
                                                                                                                                                                                                                                                                               WPI; 2003-697522/66.
                                                                                                                                                                                                                                       (MCCA/) MCCALL J D.
                                                                                                                                                                                                                                                           8
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121 AA;
                                                                                                                             WO2003068821-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S 121
                                                                                             Chimeric.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
01-FEB-1995
06-MAY-2004
                                                                                                                                                   21-AUG-2003
                                                                                                                                                                                                                                                          Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR55215;
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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80 NQKFKGKAILIADKSSSTAYMQLSSLISEDSAVYYCARSTYYGGDSYFNVWGAGTIVIVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRL---RYFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is the murine variable region heavy chain derived from murine anti-CD20 monoclonal antibody 2BS. See also AAQ65629-35. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQQPGABVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
B cell lymphoma chimeric antibody, CD20; peripheral blood cells; cell lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating B cell lymphoma with chimeric antibody - against CD20, rapid depletion of peripheral B cells, also new antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Newman RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.9%; Score 534.5; DB 2; Length 140; 83.5%; Pred. No. 8.6e-38; ive 8; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour cell; cancer; adenocarcinoma; malignancy; B9E9.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB30694 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 5; 101pp; English.
                                                                                                                                                                                                                                                     93WO-US010953.
                                                                                                                                                                                                                                                                                                     92US-00978891
93US-00149099
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rastetter WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 83.59
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces avidinii.
Homo sapiens.
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Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scPvSA; anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy; cell-specific targeting agents; single chain; tumour; B9E9.

89E9 scFvSA fusion protein A amino acid sequence.

(first entry)

09-OCT-2003

ABJ39009;

ABJ39009 standard; protein; 412 AA.

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The present sequence represents a fusion of an anti-CD20 single chain antibody (BBE9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively incleic acid encoding streptavidin or its functional variant operatively uncleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumor cells associated with cancer, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                         Schultz JE, Lin Y, Sanderson JA, Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 534.5; DB 4; Length 4:
Pred. No. 2.6e-37;
6; Mismatches 7; Indels
                                                                                  249. .253
/note= "linker"
254. .412
/note= "streptavidin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 11B; 100pp; English.
                109. .126
/note= "linker"
127. .248
/note= "VH chain"
note= "VL chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.9%;
85.2%;
                                                                                                                                                                                                                                              05-JUN-2000; 2000WO-US015595.
                                                                                                                                                                                                                                                                                 99US-0137900P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.9
Best Local Similarity 85.2
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                      (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC86563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenocarcinomas.
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                                                                                                                                                                          WO200075333-A1
                                                                                                                                                                                                                                                                                                  03-DEC-1999;
                                                                                                                                                                                                                                                                                 07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                    Goshorn SC,
                                                                                                                                                                                                           14-DEC-2000
                                                   Protein
                    Peptide
                                                                                    Peptide
                                                                                                                         Protein
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254. .412 /note= "Streptavidin region of the fusion protein"

/note= "VL region of the fusion protein"

Location/Qualifiers

Streptomyces avidinii.

Mus sp. Synthetic.

Region Region

/note= "VH region of the fusion protein" /note= "Synthetic linker region (pKOD)" 128. .247

Region

Region Region

248. .253 /note= "Synthetic linker region"

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This invention relates to novel vector constructs for the expression of streptavidin fusion proteins. Streptavidin (SA) is produced by Streptavidin fusion proteins. Streptavidin (SA) is produced by streptomyces avidinil and specifically binds water-soluble biotin. The vectors comprise a nucleic acid sequence encoding genomic streptavidin, a promoter operatively linked to the nucleic acid sequence and a cloning site for insertion of a second nucleic acid sequence encoding an anti-cD25 antibody or its antigen binding fragment. The fusion proteins encoded are known as single chain antibody-genomic streptavidin fusion conteins (SPCSA). The vectors may have cytostatic activity when used in gene therapy. The vectors may be useful in expressing genomic streptavidin fusion cassettes. The fusion proteins may be used as a reptavidin fusion cassettes. The fusion proteins may be used as treatment and the bBSB single chain antibody-genomic streptavidin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vector construct for expressing genomic streptavidin fusion proteins useful as diagnostic markers or as cell-specific targeting agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 534.5; DB 6;
Pred. No. 2.6e-37;
6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11B; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.2
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-532908/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABT43498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 412 AA;
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61 NOKPKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YPDVWGAGTTVTV 116

128

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SS 248 SS 118

RESULT 8 ABJ39009

117

187

246

11

Reno JM;

Graves SS, Schultz JE, Lin Y, Sanderson JA,

07-DEC-2001; 2001US-00013173. 17-MAY-2002; 2002US-00150762. 16-SEP-2002; 2002US-00244821.

(NEOR-) NEORX CORP.

Dearstyne EA;

Goshorn SC,

06-DEC-2002; 2002WO-US039429

WO2003050260-A2

19-JUN-2003

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Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A 140
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Rastetter WH;
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ID ABU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycan, and contacting the truncated glycan, that least one glycosyl contact of the sast one glycosyl transferase and at least one glycosyl donor under conditions suitable to transfer at least one glycosyl donor to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSP) peptide, interferon alpha peptide, interferon beta peptide, Factor VIII peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI) peptide, interferon-gamma peptide, tissue plasminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, Pactor VIII peptide, TMFalpha receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-Glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti-HER2
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                                                                                                                    246
                                                                                NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGAGTTVTV 116
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remodeling a peptide, by removing a saccharyl subunit from the peptide form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the
                   188 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTV
QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bayer R, Bowe C, Hakes D, Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-CD20 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                       ABR55873 standard; protein; 140 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0328523P.
2001US-0344692P.
2001US-0334233P.
2002US-0334301P.
2002US-039177P.
2002US-039177P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEOS-) NEOSE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2002; 2002WO-US032263
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-449162/42.
N-PSDB; ACC78895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide remodeli:
antibody; mouse.
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                                                                                                                                                             SS 118
                                                                                                                                                                                                   SS 248
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17-JUL-2002;
16-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2001;
19-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Frees S,
                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2003
                                                                                                                                                               117
                                                                              61
                                                                                                                                                                                                     247
                                                                                                                                                                                                                                                                                                                                                 ABR55873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                 ABR55873
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Treating B cell lymphoma in humans, comprises administering immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled
antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide, insulin peptide, hepatitis B surface antigen (HbsAg), human growth hormone (HGH) peptide, and a modifying group, where the modifying group is covalently attached to the peptide through an intact glycosyl linking group. The method is useful for a cell-free, in vitro method of remodeling the above mentioned peptides. The present sequence represents the murine anti-CD20 antibody heavy chain mature variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOKFKGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 NQKFKGKATLTADKSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating B cell lymphoma. The method comprises administering at a first administration period, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VH; expression vector; murine; heavy chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                           85.8%; Score 533.5; DB 6; Length 140; 83.5%; Pred. No. 1e-37; ive 8; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20. .140
/label= Mature_anti-CD20_antibody_VH_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reff ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine anti-CD20 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU08394 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunologically active, chimeric a anti-CD20 antibodies to the human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 5; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-2001; 2001US-00911703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-352746/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABX94209.
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The invention relates to an improved method for treating B cell lymphoma comprising administering an anti-CD20 antibody. The improvement comprises administering at least one chemotherapeutic agent. The antibody causes a substantial depletion of peripheral B cells. The antibody is chimeric anti-CD20 or C2B8. The method is useful for treating B cell lymphoma. This sequence represents a murine immunoglobulin heavy chain variable region used in the method of the invention.
                                                                                                                                                                                                 61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                   1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at
                                                                                                                           1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                           OVOLOÓPGAELVKPGASVKMSCKASGYTFTSYNMHWVKOTPGRGLEWIGAIYPGNGDTSY
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating B cell lymphoma by administering an anti-CD20 antibody and
                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 533.5; DB 7; Length 140;
Pred. No. 1e-37;
8; Mismatches 9; Indels 3.
                                                      Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B cell lymphoma; anti-CD20; peripheral B cell; C2B8; immunoglobulin heavy chain variable region; mouse; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine immunoglobulin heavy chain variable region.
                                                      7;
                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newman RA,
                                                    Score 533.5; DB
Pred. No. 1e-37;
                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 11; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                  ADE85690 standard; protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    least one chemotherapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-00978891.
93US-00149099.
97US-00921060.
                                                85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.8%;
83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2002; 2002US-00238681
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-897520/82.
                                                                       Similarity
                    Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADE85689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003147885-A1
                                                                                                                                                                                                                                                                                                          A 140
                                                                                                                                                                                                                                                                      S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DR,
Rastetter WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IDEC-) IDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1992;
03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1997;
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                                                                                        Matches 101;
                                                                                                                                                                                                                                                                      118
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE85690;
                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                          140
                                                  Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to cells producing an antibody molecule specifically binding to CD20 are new, in which the antibody contains N-glycoside bond complex sugar chains bonded to the Fc region of the antibody peptide chains, of which less than 20% have a fucose residue bonded to the N-acetylglucosamine residue at the reducing end of the sugar chain. The cells are used in the treatment and prevention of cancer and immune disorders. This sequence corresponds to a protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                            61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
               administering, at a second administration period, a radiolabelled anti-
CD20 antibody, to the human subject. The invention also discloses
expression vectors that may be used in the method of the present
invention. The method is useful for treating B cell lymphoma in humans.
The present sequence represents murine anti-CD20 antibody heavy chain
variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc-bound sugar chains of low fucose immune disorders.
immunologically active, mouse/human chimeric anti-CD20 antibody and/or
                                                                                                                                                                                                                                                                        20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Б,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine; sugar chain; cancer; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakano
                                                                                                                                                                                                                  3;
                                                                                                                                                                              Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satoh M,
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-CD20 antibody heavy chain variable region
                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shinkawa T,
                                                                                                                                                                              Score 533.5; DB Pred. No. 1e-37; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant; cytostatic; antibody; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and having Fc-bound cancer and immune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 14; 200pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       저,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC66270 standard; protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uchida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002; 2002JP-00106948.
01-NOV-2002; 2002JP-00319975.
                                                                                                                                                                              85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-DEC-2002; 2002WO-JP013534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                  Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody binding to CD20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakurada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-559274/52.
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADC66269
                                                                                                                                            Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003055993-A1
                                                                                                                                                                                                                                                                                                                                                                                                  118 S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                    140 A 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shitara K,
                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                Query Match
                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC66270
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The invention relates to a drug containing as the active ingredient, an antibody composition produced by cells tolerant to a lectin recognising a gugar-chain structure in which an alpha-bond is formed between the 6-position of N-acetylglucosamine at the reducing end of an N-glycoside bond-type complex sugar chain and the 1-position of fucose. The drugs are useful in screening and treating patients not suitable for drugs not derived from these cells. They are particularly useful as diagnostics, preventives or remedies for diseases accompanying tumour, allergy or inflammation, autoimmune diseases diseases of the circulatory system, and viral or bacterial infections. In a method from the invention, a CCR4 gene was used for constructing a vector (CAG-CCR4/pcDNA3) for producing a transformant EL-4 cell (ATC TIB-39) to express chimeric CCR4. Antibody-dependent cytotoxicity of the thus produced antibody composition was confirmed. The current sequence represents a protein related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
  80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drugs containing antibody compositions produced by cells tolerant to lectin recognizing specific sugar-chain structure, useful in screening and treating patients not suitable for drugs not derived from these
                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; antiallergic; immunomodulator; cardiant; virucide; antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose; tumour; allergy; inflammation; autoimmune disease; circulatory system; viral; bacterial; infection; CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLQQPGABLVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 533.5; DB 7;
Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 13; 157pp; Japanese.
                                                                                                                                                                                                                                                                                                                                Protein related to the invention #2
                                                                                                                                                                                                 ADF60661 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2003; 2003WO-JP004503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002; 2002JP-00106949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.5%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                     (first entry)
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N-PSDB; ADF60652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shitara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 140 AA;
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                                             S 118
                                                                                        A 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to cells with modified sugar chain modifying enzyme activity. The enzyme activity of binding the 1-position of fucose to the 6-position of an N-acety/glucosamine at the reducing end of a complex N-glycoside linked sugar chain via an alpha-bond is absent or less than in the parent cell. The sugar chain modifying enzyme is preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-ADE73055). The invention is useful for the treatment and prevention of tumours, allergy, inflammation, autoimmune disease, circulatory disorders, and viral and bacterial infection. The present sequence was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                          80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                    NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial; Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour; allergy; inflammation; autoimmune disease; circulatory disorder; viral infection; bacterial infection; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cells with reduced or absent alpha 1,6-fucosyltransferase activity treatment of tumors, allergy, inflammation, autoimmune disease, circulatory disorders, and viral and bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 165-166; 187pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamano K;
                                                                                                                                                                                                                                                                                                            ADE73084 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine FUT8-related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamane N, Satoh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-833570/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB: ADE73069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 140 AA;
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This invention relates to novel erythropoietin (EPO) peptides and the remodelling and glycoconjugation of these naturally occurring peptides thereof. Specifically, each EPO peptide comprises one or more glycans and has a glycoconjugate molecule such as polyethylene glycol (EEG) attached to it. Accordingly, the present invention provides glycobEqylated EPO peptides that have either monoantennary, biantennary or triantennary glycans covalently attached thereto. As such, these peptides are useful for the treatment of anaemia, and hence exhibit antianaemic activities working to increase haematocrit levels in mammals, in particular in erythrocytes. Furthermore, EPO therapy can be used to treat kidney dialysis patients. This polypeptide is a human protein sequence related to the field of haematology, given in an exemplification of the
80 NOKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                       Mature variable heavy chain anti-CD20 murine antibody protein SegID 62.
                                                                                                                                                                                                                                                                                                     mouse; murine; antibody; erythropoietin; EPO; glycoconjugation; glycoPEGylated EPO peptide; anaemia; antianaemic; haematocrit level; kidney dialysis; haematology; CD20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel erythropoietin peptide comprising one or more glycans, having glycoconjugate molecule covalently attached to peptide, useful for treating anemia in mammal such as human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 62; 1018pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowe C,
                                                                                                                                                                    ADN49734 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bayer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2002; 2002WO-US032263.
05-NOV-2002; 2002US-00287994.
06-JAN-2003; 2003US-00367770.
19-FEB-2003; 2003US-00360779.
09-APR-2003; 2003US-00410945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2003; 2003WO-US031974
                                                                                                                                                                                                                                    15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zopf D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-399848/37.
N-PSDB; ADN49733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2004.
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ADN49734
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3; Gaps

9

20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79

1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY

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Query Match 85.8%; Score 533.5; DB 8; Length 140; Best Local Similarity 83.5%; Pred. No. 1e-37; Matches 101; Conservative 8; Mismatches 9; Indels 3;

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80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
61 NOKFKGKATLITADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
                                                                                                                                            completed: May 9, 2006, 01:25:28
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GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 9, 2006, 01:25:51; Search time 17.8788 Seconds Run on:

(without alignments) 635.031 Million cell updates/sec

US-10-700-632-7 622 Title: Perfect score:

1 QVQLQQPGAEVVKPGASVKM......EVRLRYFDVWGAGTTVTVSS 118 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

																								= 1	•					
	Description	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	neavy	Ig heavy chain pre	neavy chain	neavy	neavy chain	neavy	yamma chain V	gamma	Ig gamma chain V r	neavy		neavy	neavy chain	neavy	neavy	neavy		3 leader/Ig		g H	g heavy	g gamma chain		g heavy	g heavy	
SUMMARIES	ID	B22769	PL0089	838717	G28195	E32513	S25175	PL0208	MHMSJ5	S21810	S42184	842179	S42180	A54378	MHMS4E	T01407	F28195	C27563	866537	S20646	MHMS18	PC4402	S53751	A30577	PC1155	838950	S40295	S41394	A39276	G2MS43
	DB	73	N	~	N	N	~	~	-	~	7	7	~	~	-	~	~	~	~	~	-	4	~	N	~	~	~	~	7	П
	Query Match Length	120	119	118	120	138	120	136	117	138	101	101	102	115	117	140	120	115	131	123	139	287	116	135	133	246	446	120	141	137
d	Query Match	79.4	79.0	77.8	77.7	77.4	•	77.3	77.1	76.8	76.5	76.5	76.5	76.4	76.1	76.1	76.0	75.7	75.4	75.3	75.2	75.2	74.9	74.9	74.8	74.7	74.7	74.6	74.6	74.3
	Score	494	491.5	484	483	481.5	480.5	480.5	479.5	477.5	476	476	476	475	473.5	473.5	473	471	469	468.5	468	468	466	466	465	4.	464.5	464	464	462
	Result No.	Н	7	М	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain V region (12818-1) - mouse C;Species: Mus musculus (house mouse) C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Mar-2000 C;Accession: PL0089 R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; C A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s ar A;Reference number: PL0080; MUID:89094248; PMID:2492056

A; Molecule type: mRNA A; Residues: 1-19 <MES. A; Cross-references: UNIPARC:UPIO000115F1B; GB:X58580; GB:Y00794; NID:g51591; PIDN:CAA41 A; Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal an A; Note: sequences from two other clones (18528-16 and 12584-3) were almost identical to C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

A; Accession: PL0089

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2 JL0076	1 MHMS	2 B305	2 PH1	2 PH:	2 A2.	2 82(	2 PLO	2 A24	2 F29	2 \$03	2 538	2 \$20	2 855	2 A24'	2
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7	120 1 1	123 2 1	140 2 1	140 2 1	139 2 1	119 2 8	115 2 1	119 2 /	137 2 1	117 2 8	118 2 8	116 2 8	116 2 8	118 2 1	
74.0 141 2	73.8 120 1 N	73.7 123 2 1	73.6 140 2 1	73.4 140 2 1	73.3 139 2 1	73.2 119 2 8	73.2 115 2 1	73.2 119 2 1	73.2 137 2 1	117 2 8	73.1 118 2 8	72.9 116 2 8	72.9 116 2 8	72.9 118 2 1	

## ALIGNMENTS

RESULT B22769	RESULT 1 822769
Igh	Ig heavy chain V region (B1-8.VI/V2) - mouse (tentative sequence)
C; Sp	C;Ppecies: Mus musculus (Mouse Mouse) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C; Ac	C.Accession: B22769
K; DI	к;bilarop, к.; bruggemann, м.; кааргисл, А.; кајемѕку, к.; beyreuner, к. ЕМВО J. 1, 635-640, 1982
A;Ti	A; Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A; Re	Ajketetence number: A309/1; Mulu:04230020; FMLD:/I00333 Ajkocession: B22769
A; Mo	A; Molecule type: protein
A; Cr	A;Cross-references: UNIPARC:UP10000176B76
A; No	$A_i$ Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V
A; No	A.Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq
C; Ke	cjougertamirity: immunidy.courth; v region; immunoglobulin Cikeywords: heterotetramer; immunoglobulin
F;15	F;15-98/Domain: immunoglobulin homology <imm></imm>
g	Query Match 79.4%; Score 494; DB 2; Length 120;
Be	Best Local Similarity 77.5%; Pred. No. 4.7e-37; Matches 93; Conservative 11; Mismatches 14; Indels 2; Gaps 1;
ò	1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYXIHWIKQTPGQGLEWVGVIYPGNDDISY 60
q	1 QVQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNY 60
ò	61 NOKFKGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118
qq	61 NQKFKGKATLITVDKPSSTAYMQLSSLTSEDSAVTYCARYDYYGSSYFDYWGQGTTLITVSS 120

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A;Cross-references: UNIPARC:UP100001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin munoglobulin homology C;Reywords: heterotetramer; immunoglobulin homology <IMM>
P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                             Ig heavy chain precursor V region (MRL22) - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C;Accession: B32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest: 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: E32513
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP10000114D9D; GB:M20835; NID:g196945; PIDN:AAA38847.1; PID. C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keyworfas: heterotetramer; immunoglobulin munoglobulin homology C;Keyworfas: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ighavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain C;Species: Mus musculus (house mouse)
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C;Accession: E10208
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEKFKGKATLIADKSSSTAYMQLSSLTSEDSAVYFCAREGSYEYDEADYWGXGTTLTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region - mouse
Cispecies: Mus musculus (house mouse)
Cibate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Cibacession: 825175
R;Monsetier: M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Bubmitted to the EMBL bata Library, July 1992
a;Description: Structure and binding properties of monoclonal antibodies to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNIDPSDSETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGKATLIADDKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYF--DVWGAGTTVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOKFKGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREV---RLRYFDVWGAGTTVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.4%; Score 481.5; DB 2;
75.8%; Pred. No. 7e-36;
iive 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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75.8%; Pred. No. 7.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
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Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-138 < KOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-120 < MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S25175
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
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Best Local Si
Matches 91
  61
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(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Spacies: Mus musculus (house mouse)
(Spacession: G28195
(Spacession: G28195
(Spacession: G28195)
(Spacession: G28195)
(Species: M.B. M.A.; Deans, R.J.; Bolger, M.B. M.F.
(Species: M.A.; Deans, R.J.; Bolger, M.B. M.F.
(Species: Muscule binding to monoclonal antibodies. Hypervariable region amino acid shaperace number: A28195; MUID:88153717; PMID:3267217
(Speciession: G28195
(Speciession: G28195
(Speciession: G28195)
(Speciession: G28195)
(Speciession: MIPPARC:UPI0000114D6F; GB:M19772; NID:g195520; PIDN:AAA38340.1; PID:G.
(Superfamily: immunoglobulin nomology
(Speciession: immunoglobulin homology < IMM)
(Speciession: immunoglobulin homology < IMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Reference number: S38713
A,Accession: S38717
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-118 <CIM>A,CEOSSION: NID:g416099; PIDN:CAAS3607.1,
A,CEOSSION: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38717
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDQLQQSGPDLVXPGASVKMSCKASGYTFTNYVIHWVKQRPGQGLEWIGYIHPYNDGSKX
                                                                                                                                     QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYTHWIKQTPGQGLEWVGVIYPGNDDISY
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                         Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
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           Query Match
Best Local Similarity 78.2%; Pred. No. /.oc. ...
Marches 93; Conservative 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.7%; Score 483; DB 2; 76.7%; Pred. No. 4.5e-36; iive 10; Mismatches 16;
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Best Local Similarity
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Best Local S:
Matches 91
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BALB/c)

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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Readues: 1-138 <OST>
A;Cross-references: UNIPARC:UPI0000115ED6; EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PI
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A;Residues: 1-101 <MOJ-3
A;Cross-references: UNIPARC:UP1000011655F; EMBL:Z25447; NID:g407816; PIDN:CAA80934.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                         immunoglobulin homology
                                                                                                                                                                 A; Introns: 15/3
C; Superfamily: immunoglobulin V region; immunog
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
       A; Reference number: S21810
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Best Local Similarity
Matches 88; Conserv
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Best Local Similarity
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A; Residues: 1-101 < MOJ>
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Matches
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Datcession: A26242
R;Schilling, J; Clevinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangemente
A;Reference number: A26242; MUD:80078170; PMID:6765983
A;Reference number: A26242; MUD:80078170; PMID:6765983
A;Residues: 1-117 <SCH>
A;Molecule type: protein
A;Residues: 1-117 <SCH>
A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that C;Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IM>
F;22-96/Disulfide bonds: #status predicted
ol. Immunol. 27, 429-433, 1990
Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reactin
Reference number: PL0207; MUID:90309764; PMID:1973259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cha
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submitted to the EMBL Data Library, January 1991
A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
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                                                                                                                                                                   A; Experimental source: hybridoma cell E225
C; Superfamily: immunoglobulin V region; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 480.5; DB 2
; Pred. No. 8.5e-36;
16; Mismatches 13
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78.0%; Pred. No. 8.9e-36;
iive 10; Mismatches 15
                                                                                                                                                                                                                                                            F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;118-121/Region: Dregion
                                                                                                                                                                                                                                             F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                             A; Cross-references: UNIPARC: UPI0000176C6F
                                                                                                                                                                                                                                                                                                                                                                                                              77.3%;
74.6%;
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Best Local Similarity
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nes 92; Conserv
                                                                                                   A; Molecule type: mRNA
A; Residues: 1-136 <SOU>
                                                                          Accession: PL0208
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Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 06-Jun-1997
C;Accession: 842184
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Birr, J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with specasion: S42184
A;Accession: S42184
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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: 842179
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Ehr. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with specific respinance: 542176; MUID:94009207; PMID:7691608
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   Length 138;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
th 76.8%; Score 477.5; DB 2; Length I Similarity 76.5%; Pred. No. 1.6e-35; 91; Conservative 10; Mismatches 17; Indels
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A;Status: translated from GB/EMBL/DDBJ
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77.1%;
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 542180
C;Accession: 542180
C;Accession: 542180
C;Accession: 542180
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with specta, A;Reference number: 542176; MUID:94009207; PMID:7691608
A;Accession: 542180
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R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
A; Rici Chem. 269, 7019-7023, 1994
A; Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc A; Reference number: A54378; MUID:94165109; PMID:7509814
A; Accession: A64378
A; Accession: A64378
A; Residues: preliminary
A; Residues: preliminary
A; Residues: 1-115 c.AGA>
A; Residues: 1-110 multipation of myeloma cell line MOPC 315.43
A; Note: sequence attracted from NCBI backbone (NCBIN:144172)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin c; Reywords: heterotetramer; rewords: heterotetramer; rewords: heterotetramer; rewords: heterotetramer; rewords: heterotetramer; rewords: heterotet
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C;Species: Mus musculus (house mouse)
C;Date: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
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                                                                                                                          Query Match 76.5%; Score 476; DB 2; Best Local Similarity 90.7%; Pred. No. 1.6e-35; Matches 88; Conservative 5; Mismatches 4
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C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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tes 88; Conservative
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Gaps

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A; Molecule type: protein
A;Residues: 1-17 <KEH>
A;Cross-references: UNIPARC:UPI0000270F1
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context & C;Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
F;22-96/Disnlfide bonds: #status predicted
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical
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C;Species: Mus sp. (mouse)
C;Acres: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T01407
R;Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitch, S.; Onishi, S.; Yamamot
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A,Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A,Reference number: Z14317; MUID:93116638; PMID:1474935
                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02039
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain A;Reference number: A02039; MUID:83075344; PMID:6816276
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QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
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A,Residues: 1-140 -7AK>
A,Crosidues: 1-140 -7AK>
A,Crosidues: 1-140 -7AK>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
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Search completed: May 9, 2006, 01:33:51 Job time : 18.8788 secs

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Name=IgG1 anti-TS1 VV;

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Muridae; Mutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

NCBI_TaxID=10090;
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Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;

Studies of the interactions between the anticytokeratin 8 monoclonal antibody TSI, its antigen and its anti-idiotypic antibody alphaTSI.";

J. Mol. Recognit. 16:157-163(2003).
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Pred. No. 4.2e-45;
8; Mismatches 12; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; Ada4574; CA156336.1; -; mRNA.
InterPro; IPR001559; Ig.
InterPro; IPR001559; Ig.
InterPro; IPR001559; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR00406; Ig.
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04VAB6 MOUSE
0924R1 MOUSE
0924R2 MOUSE
0924R2 MOUSE
0924Q3 MOUSE
090DC9 MOUSE
099BL4 MOUSE
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Q924P6 MOUSE
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     0924R0 MC
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D 091067_MOUSE PRELIMINARY; PRT;
AC 091067;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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QSF211;
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921VA2 MOUSE
HV12 MOUSE
958JZ2 RAT
921C4 MOUSE
921C4 MOUSE
924F5 MOUSE
924Q1 MOUSE
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Q924Q0_MOUSE
Q924Q5_MOUSE
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HV13_MOUSE
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HV11_MOUSE
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Q924P8_MOUSE
Q9JL75_MOUSE
Q924Q4_MOUSE
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Gapop 10.0 , Gapext 0.5
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PIR; PHI150; PHI150.
PIR; PHI151; PHI51.
PIR; PHI152; PHI51.
PIR; PHI153; PHI53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVOLQOPGAEVVKPCASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
Mame-VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                  A KOZONO Y., KOZONO H., AZUMA T.;
SUBMITCED (ANG-2001) to the BMBL/GenBank/DDBJ databases.
SUBMITCED (ANG-2001) to the BMBL/GenBank/DDBJ databases.
R EMBL; AB069912; BAB63928.1; -; mRNA.
R EMBL; AB069914; BAB63930.1; -; mRNA.
R PIR; S26744; S26744.
R HSSP; P01751; 1A8.
R EMBL; AB069014; BAB63930.1; -; mRNA.
R RSWUSGOOO00021155; Mus musculus.
R InterPro; IPRO07110; Ig-like.
R InterPro; IPRO07110; Ig-like.
R SWART; SM04406; IGV; 1.
R RNART; SM04406; IGV; 1.
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Submitted (AUG-2011) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069915; BAB63931.1; -; mRNA.
PIR; PH1159; PH1159.
HSSP: P01751; 1A6W.
SNR; O924Q0; 1-134.
Ensembl; ENSWIGG0000021155; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00895; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.6%; Score 495; DB 2; Length 14 Best Local Similarity 78.8%; Pred. No. 9.6e-45; Matches 93; Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15704 MW; C99D2433F2BAD8A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2001 (TrEMBLrel. 26, Last annotation update)
V165-D-J-C mu protein (Fragment)
Name=V165-D-J-C mu;
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Q924Q0;
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                                                                                                          1 QVOLOQPGAEVVKPCASVKMSCKASGYTFTSYXIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murines, Mus.
                                                          0; Gaps
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Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of 57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
gpecific V genes as the original antigen.";
J. Immunol. 141:779-784(1988).
EMBL; AB067795; BAB63280.1; -; mRNA.
PIR; F28833; F28833.
Query Match 79.3%; Score 493; DB 2; Length 143; Best Local Similarity 78.0%; Pred. No. 1.6e-44; Matches 92; Conservative 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sec
01-OCT-2003 (TrEMBLrel. 25, Last and
VH186.2-D-J-C mu protein (Fragment)
Name=VH186.2-D-J-C mu;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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ID Q924Q5 MOUSE PRELIMINARY;
AC Q924Q5;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lischul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones E.D., M., Marra M.A.;

Rodriguez A.C., Grimwood S.J.M., Marra M.A.;

Rodriguez A.C., Grimwood S.J.M., Marra M.A.;

Rodriguez A.C., Schein J.E., Jones E.D., W., Marra M.A.;

Rodriguez A.C., Schein J.E., Jones E.D., Smailus D.E.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.;

Rodriguez A.C., Schein J.E., Jones E.D., Smailus D.E.,

Rodriguez A.C., Schein J.E., Jones E.D., Swailus D.E.,

Rodriguez A.C., Swailus J. Jones E.D., Swailus J. Jones
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                                                                    1 QVQLQQPGAEVVXPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                      1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2464031;
Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
Morrison S.L., Kabat E.A.;
"Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1---6)dextrans.";
J. Immunol. 142:888-893(1989).
BMBL; BC018315; AAH18315.1; -; mRNA.
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78.6%; Score 489; DB 2; Length 143;
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Ensembl; ENSMUSG0000054328; Mus musculus.

Ensembl; ENSMUSG00000054328; Mus musculus.

Ensembl; ENSMUSG1000050136.6.

GO; GO:0019815; C:B cell receptor complex; IDA.

GO; GO:0008997; C:external side of plasma membrane; IDA.

GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.

GO; GO:0048471; C:perinuclear region; IDA.
                                   Indela
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                  Pred. No. 4.2e-44;
10; Mismatches 17;
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STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                        Created)
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                77.1%;
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Q8VCX7;
                                 91; Conservative
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NCBI_TaxID=10090;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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-I- MISCELLANEOUS: This protein binds dextran.
-I- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%; Score 484; DB 2; Length 61.
76.3%; Pred. No. 8e-43;
ive 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
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InterPro; IPR003596; Ig v.
SMART; SM00406; IGv; 1.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                       1; Gaps
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Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                               DB 1; Length 117;
                                                                                                                                                                                                                Query Match
Best Local Similarity 78.0%; Pred. No. 3.4e-43;
Best Local Similarity 78.0%; Pred. No. 3.4e-43;
Matches 92; Conservative 10; Mismatches 15; Indels
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O.7072.2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Al324046.
Name-Al324046;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
DOMAIN I 116
IG-like.
                                                                               Ig-like.
By similarity.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
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HSSP; P01865; 1KBS.
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Q7TWK1;
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NON TER
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61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAR---EVRLRYFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NQKFKGKATLITVDKSSSTAYMELNSLISEDSAVYXCARYYYSGSYWYFDVWGAGTTVTVS 139
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                                                                                                                                                                                                                                                                                                                  1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                               Query Match 77.1%; Score 479.5; DB 2; Length 470; Best Local Similarity 74.4%; Pred. No. 1.8e-42; Matches 90; Conservative 13; Mismatches 15; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067782; BAB63267.1; -; mRNA.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl_set; 3.
SMART; SM0406; IGv. 1.
PROSITE; PS00290; IG_IKE; 4.
Hypochetical protein; Immunoglobulin domain.
SEQUENCE 470 AA, 51728 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15648 MW; 51894D22EA9FDD47 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
VM1466.2-D-J-C mu protein (Fragment).
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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PH1108;
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RA Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;

RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of Stallogeneic manipulation of the GAT idiotypic cascade. Immunization of Stallogeneic manipulation of the GAT idiotypic cascade. Immunization of Stallogeneic world. Stallogeneic manipulation of Stallogeneic manipulation of Stallogeneic Stall
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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                                                                                                                                                                                                                         DB 2; Length 145;
                                                                                                                                                                                                                   ;; Score 476; DB 2; Length 14;; Pred. No. 1e-42;
11; Mismatches 16; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA
PIR; S26744; S26744.
HSSP; P01751; 1A6W.
SWR; Q924R3; 1-136.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SW00406; IGv; 1.
                                                                                                                                                                                                                       76.5%;
75.8%;
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Q924R8;
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PubMed=3135311;
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SEQUENCE
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                                                                                                                                       1 OVOLOOPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
                                                                                                                                                                               61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118
                                                                                                                                                                                                  Kartinen M., Rocca-Serra J., Makela O.;
"Combinatorial association of V genes: one VH gene codes for three mon-cross-reactive moncolonal antibodies each specific for a different antigen (phoxazolone, NP or gat).";
Mol. Immunol. 25:859-865(1988).
BENEL; AB067787; BAB63272.1; -; mRNA.
PIR; PAB067787; BAB63272.1; -; mRNA.
PIR; PH1105; PH1105.
PIR; PH1105; PH1108.
PIR; PH1114; PH1114.
PIR; PH1119; PH1119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=3135311;
Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
J. Immunol. 141:779-784(1988).
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muridae, Murinae, Mus.
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                                                              Gaps
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                      Length 143;
                77.0%; Score 479; DB 2; Length 14
75.4%; Pred. No. 4.9e-43;
ive 11; Mismatches 18; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH186.2-D-0-C mu protein (Fragment)
Name=VH186.2-D--C mu;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                         PRT;
      Query Match
Best Local Similarity 75.4%
                                                                                                                                                                                                                                                                                                                       Q924R3_MOUSE PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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PH1126.
PH1128.
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PH1137.
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PH1126; 1
PH1128; 1
PH1129; 1
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PH1134;
PH1137;
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PH1147;
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PH1151;
PH1152;
PH1153;
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PIR;
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143 AA; 15617 MW; 51952152P6F3AD47 CRC64;
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HSSP; P01751; 1NQB.
SMR; P01756; 1-117.
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Best Local Similarity
                            Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                          HV12 MOUSE
P01756;
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   SEQUENCE
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                                                                                                                                                                                                                                                                                                                1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
VH186.2-D-J-C mu procein (Fragment).
Name-VH186.2-D-J-C mu;
Mus muscullus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                             1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kozono Y., Kozono H., Azuma T.;
Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABN677986; BAB62271.1; -; mRNA.
EMBL; ABN69911; BAB63927.1; -; mRNA.
                                                                                                                                                                  146 146
146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
                                                                                                                                                                                                                   Query Match 76.4%; Score 475.5; DB 2; Best Local Similarity 74.4%; Pred. No. 1.2e-42; Matches 90; Conservative 11; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA
PIR; PH1153; PH1153.
HSSP; PO1751; LAGW.
SMR; O24488; 1-137.
Ensembl; ENSWUSGO0000021155; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus
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Ensembl; ENSMUSG0000021155; Mus
                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR001356; Ig-v.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q91VA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PH1105; PH1105.
PH1114; PH1114.
PH1118; PH1118.
PH11125; PH1125.
PH1125; PH1125.
PH1126; PH1126.
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PH1137.
PH1142.
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STRAIN=C57BL/6;
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PH1152; PH1152.
; P01751; 1A6W.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                   1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
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                                                                                                                                                                                                                                                                  61 NEKFKSKATLITVDKPSSAAYMQLSSLTSEDSAVYYCAKRSNYGAFDVWGTGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma protein has also been determined.
-!- MISCELLANEOUS: This protein binds dextran.
-!- SIMILARITY: Contains I Ig-like (immunoglobulin-like) domain.
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS5035; IG_LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Immunoglobulin V region.
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N-linked (GlcNAc. . .) (complex)
By similarity.
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ch 76.2%; Score 474; DB 2; Length 143; I Similarity 74.6%; Pred. No. 1.7e-42; 88; Conservative 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 55 N-linked (GlcNAC. .) (cc
22 96 By similarity.
117 117 AA; 12983 MW; 3CP8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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118 $ 118
                          136 S 136
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                                                                                  MOUSE
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                                                                                                                                                                                                                                          TISSUE-Thymus;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

B Diatcherco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Muhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Notiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYF---DVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOKFNGKATLIADKSSSTAYMOLSSLISEDSAVYFCARD----YFDGYDYWGQGVMVTVS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLQQSGAELVKPGSSVKISCKASGYTFTNYDIHWIKQQPGNGLEWIGMIYPGNGNTKY 79
                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Buarchontoglires, Glires; Rodentia; Sciurognathi;
Muroidea, Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
-!- SUBCELLUIAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 472.5; DB 2; Length 458; 76.0%; Pred. No. 9.6e-42; ive 9; Mismatches 13; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR01359; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.cl.
InterPro; IPR003596; Ig.cl.
InterPro; IPR004095 IG.3
SMART; SM00409; IG.3
SMART; SM00406; IGV; 1.
PROSITE; ES50835; IG.LIKE; 4.
Immunoglobulin domain; Repeat.
SEQUENCE 458 AA; 50161 MW; AOAGIDCDD2CA433E CRC64;
                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                         458 AA.
                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC091272; AAH91272.1; -; mRNA.
SMR; Q5BJZ2; 21-454.
                                                                   10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.
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Matches 92; Conservative
                                         PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                               LOC367586 protein.
                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thymus;
NIH MGC Project;
                                                                                                                             Name=LOC367586;
                                         OSBJZ2 RAT
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                        Q5BJZ2 RAT
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1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYFDYWGQGTTLTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97456619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4; Mueller J.P., Glannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P., Matis L.A., Evans M.J., and M.J., Hartman S.L., Elliott E.A., Squinto S.P., Humanized porcine W.GM-specific monoclonal antibodies with chimeric 19G2/G4 constant regions block human leukocyte binding to porcine endothelial cells."; Mol. Immunol. 34:441-452(1997).

Mol. Immunol. 34:441-452(1997).

EMBL: U78801; AAD00293.1; -; mRNA.
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment)
Mus musculus (Mouse).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 75.9%; Score 472; DB 2; Length 11 1 Similarity 73.7%; Pred. No. 2.2e-42; 87; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6;
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                118 AA.
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Ensembl; ENSMUSG0000021155; Mus musculus.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS_MOUSE
Q924PS_MOUSE PRELIMINARY;
Q924PS;
Q9Z1C4_MOUSE PRELIMINARY;
Q9Z1C4;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Search completed: May 9, 2006, 01:32:36 Job time : 109.039 secs

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Sequence Sequence Sequence Sequence

Sequence Seq

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APPLICANT: ANDERSON, DARRELL R.
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: HEGNARD, JOHN E.
APPLICANT: REFF MITCHELL E.
APPLICANT: REFF MITCHELL E.
APPLICANT: REFF MITCHELL E.
APPLICANT: RESTETTER, MILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA.
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible:
GOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPLING DATE: 07-UN-1995
FILING DATE: 07-UN-1993
FILING DATE: 10-NOV-1993
FILING DATE: 11-NOV-1993
FILING DATE: 11-NOV-1993
FILING DATE: 13-NOV-1992
ATTOREY/AGENT INFORMATION:
MANE: TESKIN FORMATION:
NAME: TESKIN FORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TYPE: Amino acid
US-08-428-257A-72
US-08-491-988-3
US-08-491-988-9
US-08-491-988-9
US-08-491-988-5
US-08-491-988-5
US-08-236-520-9
PCT-US95-05262-9
PCT-US95-05262-7
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US-10-092-246-11
US-10-092-246-11
US-10-096-246A-11
US-10-096-246A-11
US-10-096-246A-11
US-10-096-246A-11
US-10-096-246A-11
US-08-913-555-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/08475815B; Patent No. 6399061; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, At Sequence 7, At Sequence 4, At Sequence 44, A Sequence 41, At Sequence 11, At Sequence 18, A Sequence 12, A Sequence 18, A Sequence 12, A Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11,
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                              GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(/cgn2_6/ptodata/1/iaa/5_COMB.pep:*

!: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

!: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

!: /cgn2_6/ptodata/1/iaa/PCTMS.COMB.pep:*

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US-09-238-741-4
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US-08-476-813-6
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PCT-US93-11612-7
PCT-US93-11612-4
US-09-579-378A-4
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US-09-419-788-113
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US-08-403-886-174A-42
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US-09-403-439-38
US-08-533-497A-12
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US-08-353-400-33
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US-08-913-555-15
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Maximum Match 100%
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Perfect score:
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Maximum DB E
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No.
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84.5%; Score 525.5; DB 1;
82.6%; Pred. No. 9.8e-42;
iive 8; Mismatches 10;
TITLE OF INVENTION: Therapeutic Application TITLE OF INVENTION: Radiolabeled Antibodies TITLE OF INVENTION: Differentiation Antigen TITLE OF INVENTION: Lymbhoma NUMBER OF SEQUENCES: 11 CORRESPONDENCES: 11 CORRESPONDENCE ADDRESSE: STREET: 699 Prince St.
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08475813
Patent No. 6682734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 amino acids
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Best Local Similarity 82.6
Matches 100; Conservative
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LENGTH: 140 amino acio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                        CITY: Alexandria
                                                                                                                                                                                                USA
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US-08-475-813-6
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                                                                                                                                                              20 QVQLQQPGAELVKPGASVKASCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                        1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                              Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BRASILAWSKY, GARY R.
APPLICANT: HANNA, NABIL
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: LABARRE, MICHAEL J.
APPLICANT: HUYNH, TRI B.
TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
FILE REFERENCE: 2352.0584
CURRENT PRILIG DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.8%; Score 533.5; DB 2; Best Local Similarity 83.5%; Pred. No. 6.5e-42; Matches 101; Conservative 8; Mismatches 9;
                                                        Query Match 85.8%; Score 533.5; DB 2; Best Local Similarity 83.5%; Pred. No. 1.8e-42; Matches 101; Conservative 8; Mismatches 9;
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Hanna, Nabil
Leonard, John B.
Newman, Roland A.
Reff, Mitchell B.
Rastetter, William H.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09238741
Patent No. 6897044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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  MOLECULE TYPE: protein
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        ; MOLECULE :::
US-08-475-815B-11
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LENGTH: 470
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APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma Therapeutic Application of Chimeric and Radiolabeled Antibodies to Human B Lymphocyte Restricted Differentiation Antigen for the Treatment of B-Cell ij 20 QVQLQQPGAELVKAGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79 9 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY Gaps 3; DB 1; Length 140; Indels OPERATION SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-5UN-1995
CLASSIFICATION NUMBER: US/08/476,275
FILING DATE: 07-5UN-1995
FILING APPLICATION NUMBER: US/08/149,099
FILING DATE: 03-NOV-1993
PROR APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:

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61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGAGTTVTVS 117
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BENDER FOLOS/MS-DOS
SOPFWARR: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.3%; Fred. No. 2.1e-4v;
Matches 96; Conservative 11; Mismatches 11; Indels
Matches 96; Conservative 11; Mismatches 11; Indels
                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                            PRIOR APPLICATION: 424
PRIOR APPLICATION 1943
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505
   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: 121 amino acids amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                             FILING DATE: 27 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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PCT-US93-11612-7
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Patent No. 6210671

GENERAL INFORMATION:

TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One MarketPlaza, Steuart Tower, Suite 2000
CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLEM PC compatible
CORRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/475,813
FILING DATE: 07-JUN-1995
CLIASSIFICATION: DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENGUNICATION NUMBER: 35,030
RESERVENCENCON NUMBER: 35,030
RESERVENCON NUMBER: 35,030
RESERVENCON NUMBER: 35,030
RESERVENCENCON
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Pred. No. 9.8e-42;
8; Mismatches 10
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St.
STREET: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.6%;
Matches 100; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES: 11
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US-08-579-378A-7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.1%; Score 510.5; DB 4; Length 121; Best Local Similarity 79.3%; Pred. No. 2.1e-40; Matches 96; Conservative 11; Mismatches 11; Indels 3.
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Sequence 14 Application PC/TUS9311612
Sequence 14 Application:
Sequence 14 Application:
Sequence 14 Application:
Sequence 15 Sequence:
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: One Market Plaza, Steuart Tower, Suite 2000
STREET: One Market Plaza, Steuart Tower, Suite 2000
STREET: One Market Plaza, Steuart Tower, Suite 2000
STATE: California
COUNTRY: USA
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
SOFTWARE: PLOPPY disk
COMPUTER: IBM PC compatible
SOFTWARE: PLOPPY disk
COMPUTER: ELACHTIN STEER:
SOFTWARE: PLOPPY disk
CURRENT APPLICATION DATA:
STEER: PLOPPY DATA:
SOFTWARE: 
                     FILING DATE:
CLASTRICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFENSINGL/OCKET NUMBER: 11823-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
APPLICATION NUMBER: PCT/US93/11612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 07/983,946
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,
APPLICATION NUMBER: US 07/983,
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William N.
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-326-24
TELEFAX: 415-326-2422
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MOLECULE TYPE: protein
PCT-US93-11612-7
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STRANDEDNESS: si
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61 NOKFKGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR----YFDVWGAGTTVTV 116
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                                                                                                                                                                                                                                         61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                       20 QAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY
                                                                                                                                                                                             20 BVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQCLEWIGYIYPYNDGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                              1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                 Gaps
                                                                                                                                                 3;
                                                                                                                    DB 4; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.9%; Score 503; DB 2; Length 140; 79.3%; Pred. No. 1.2e-39; ive 7; Mismatches 14; Indels
                                                                                                                Query Match
82.1%; Score 510.5; DB 4; Length 1
Best Local Similarity 79.3%; Pred. No. 2.4e-40;
Matches 96; Conservative 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
         SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96; Conservative
INFORMATION FOR SEQ ID NO:
                                                                    MOLECULE TYPE: protein PCT-US93-11612-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Mus musculus
US-09-724-138-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  118 $ 118
                                                                                                                                                                                                                                                                                                                                 S 140
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80 NEKFKGKATLITSDKSSSTAYMELSSLTSEDSAVYYCAREEYGNYVRVFDVWGAGTTVTVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EVOLOQSGPDLVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYIYPYNDGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SACK, Markus
APPLICANT: SACK, Markus
APPLICANT: SACK, Markus
APPLICANT: Montael
APPLICANT: Machael
APPLICANT: SPIEGEL, Holger
APPLICANT: ELRAO, Yu-Gari
APPLICANT: ELRAO, Nodecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: MOMBER: 1899-10-18
TITLE OF INVENTION: NUMBER: 98 11 9630.6 BP
EARLIER APPLICATION NUMBER: 98 11 9630.6 BP
EARLIER PILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;; Score 502.5; DB 2;
;; Pred. No. 1.4e-39;
11; Mismatches 12.
                                                                   CLASSIPICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Libesecheutz, Joe 0.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELEPROMENT CATION INFORMATION:
TELEPROMENT: 415-326-2400
                             APPLICATION NUMBER: US/08/579,378A FILING DATE: 27-DEC-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, Application US/09419788; Patent No. 6825325; GENERAL INFORMATION: APPLICANT: FISCHER, Rainer; APPLICANT: SCHILLBERG, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.8%;
78.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 140 amino acids
amino acid
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Best Local Similarity 78.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-579-378A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-09-419-788-113
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                                                                                                                                                                                                                 APPLICANT: Robinson, Randy
APPLICANT: Liu, Alvin
APPLICANT: Ledbetter, Jeffrey
TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti
FILE REFERENCE: PPL-OOLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGAGTTVTV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAYLQQSGAELVRPGASVKASCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDISY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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Patent No. 6210671

GENERAL INFORMATION:

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

TITLE OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One MarketPlaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 503; DB 2; Length 140; 79.3%; Pred. No. 1.2e-39; Live 7; Mismatches 14; Indels
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ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                         PILE REFERENCE: FFL-UOLUCU
CURRENT APPLICATION NUMBER: US/09/630,198
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 09/021934
PRIOR PILING DATE: 1998-02-12
PRIOR PILING DATE: 1998-02-12
PRIOR PILING DATE: 1995-06-06
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR APPLICATION NUMBER: US 07/195961
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1986-05-13
PRIOR PILING DATE: 1986-05-13
PRIOR PILING DATE: 1986-05-13
PRIOR PILING DATE: 1986-10-37
SOFTWARE: PCT/US86/02269
PRIOR PILING DATE: 1986-10-27
SOFTWARE: PATENTIN NUMBER: DCT/US86/02269
PRIOR PILING DATE: 1986-10-27
PRIOR PILING DATE: 1986-10-27
PRIOR PILING DATE: 1986-10-27
                                                                                             3-09-630-198-44
Sequence 44, Application US/09630198
Patent No. 6893625
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Best Local Similarity 79.33
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
US-09-630-198-44
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Robinson
APPLICANT: Liu, Al'
140 S 140
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US-08-579-378A-4
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61 NOKFKGKATLITADKSSTTAYMOLSSLITSEDSAVYYCARE-VRLRY---FDVWGAGTTVTV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%; Score 493; DB 1; Length 273; 78.5%; Pred. No. 2.2e-38; ive 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: A35
PRICK APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INPOMMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara B.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 16786/189/CHAC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                 ; Sequence 18, Application US/08403853; Patent No. 5844094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LEWETH: 273 amir.
                                                                                                                                                                                                           HUDSON, Peter J.
LAH, Maria
                                                                                                                                                                                                                                                KORRT, Alex A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 78.5
nes 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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STREET: 30
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                                                                                                                                    US-08-403-853-18
                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                     61
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Matches
                                                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                      61 NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                 1 OVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic,
CHER INFORMATION: natural origin
05-09-419-788-113
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,350B
FILING DATE: 13-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30414-20003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.4%; Score 500; DB 2; 78.8%; Pred. No. 1.9e-39; iive 10; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08766350B
Patent No. 6349244
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acids
                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 78.8%
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-766-350B-48
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SEQ ID NO 113
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Gaps 4

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162 QVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYIYPYNDGTKY 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.5%; Score 488.5; DB 1; Length 274; 78.0%; Pred. No. 5.7e-38; Live 9; Mismatches 12; Indels 5.
                                                                                                                                                                              DOS Text
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS TE
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
FULLATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
PRIOR DATE: OCCODER 16, 1995
FILING DATE: AGGRET 14, 1996
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 9, 2006, 01:35:40 Job time : 26.5628 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78.0%
Marches 92; Conservative
                                                    COUNTRY: UNITED STATES ZIP: 20005-3918
COMPUTER READABLE FORM:
       WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-860-174A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKGKATLIADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118
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APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Brik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New YORK Avenue, N.W.
STREET: 9th Floor, East Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08860174A
Sequence 12, Application US/08860174A
Sequence 12, Application US/08860174A
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Brik
APPLICANT: VERHOBIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT;
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE;
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: PILLSBURK;
STREET: 91h Ploor, Bast Tower
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Best Local Similarity 78.0%; Pred. No. 2.6e-38;
Matches 92; Conservative 9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS TEN
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
                                                                                                                     Sequence 4, Application US/08860174A Patent No. 5989810 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UNITED STATES
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  143 S 143
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Wed May 10 09:27:24 2006
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Sequence 7, Application US/10700632
Publication No. US20050118183A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
THOR APPLICATION NUMBER: US 60/424,332
PRIOR APPLICATION NUMBER: US 60/424,332
PRIOR APPLICATION NUMBER: US 60/424,332
NUMBER OF SEQ ID NOS: 94
SOPTWARE: Patentin version 3.2
TENTING DO NOS: 94
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US-10-00-632-73

Sequence 73, Application US/10700632

Sequence 73, Application Wo. US20050118183A1

Sequence 73, Application No. US20050118183A1

GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.

TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

TITLE OF INVENTION: LEUKEMIA USING THE SAME

TITLE OF INVENTION: US/10/700,632

CURRENT APPLICATION NUMBER: US/0/24,332

CURRENT APPLICATION NUMBER: US 60/424,332

PRIOR APPLICATION NUMBER: US 60/424,332

PRIOR PRILING DATE: 2002-11-07

NUMBER: OF SEQ ID NOS: 94

SEQ ID NO 73

SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVSS 118
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               US-11-019-180-4
US-11-004-639-40
US-11-004-639-44
US-11-004-639-44
US-11-004-639-46
US-11-004-639-48
US-11-004-639-48
US-11-03-6-703-48
US-10-36-709-35
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US-10-917-599-1
US-10-917-599-1
US-10-917-599-1
US-10-917-599-1
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Best Local Similarity 100.
Matches 118; Conservative
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ORGANISM: Mus musculus
US-10-700-632-7
RESULT 1
US-10-700-632-7
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556.303 Million cell updates/sec
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Sequence 4
Sequence 5
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622
1 QVQLQQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTTVTVSS
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                                                                                                                      May 9, 2006, 01:57:07; Search time 88.6277 Seconds
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/cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US1OA_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US1OB_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US1OB_PUBCOMB.pep:*
                 GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
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US-10-700-632-73

US-10-366-703-39

US-10-150-700-639

US-10-150-706-65

US-10-150-762-6

US-10-150-762-6

US-10-411-03-62

US-10-411-03-62

US-10-411-03-62

US-10-411-03-62

US-10-410-997-62

US-10-410-997-62
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length
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Result No.

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61 NOKFKGKATLITADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
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                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                    Description of Artificial Sequence: Synthetic heavy chain cA20VH amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain OTHER INFORMATION: antibody-genomic streptavidin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10013173

Sequence 6, Application US/10013173

Publication No. US2030095977A1

GENERAL INFORMATION: Stephen C.

APPLICANT: Genera, Scott Stoll

APPLICANT: Schultz, Joanne Elaine

APPLICANT: Lin, Yukang

APPLICANT: Reno, John M.

TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 690022.5470

CURRENT APPLICATION NUMBER: US/10/013,173

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 69

SOFTWRE: PastSEQ for Windows Version 4.0

SEG ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.9%; Score 534.5; DB 4; Length 412; Best Local Similarity 85.2%; Pred. No. 2.6e-40; Matches 104; Conservative 6; Mismatches 7; Indels 5.
                                                                                                                                                                                                               86.3%; Score 536.5; DB 4; Length 121; 84.3%; Pred. No. 4.6e-41; ive 6; Mismatches 10; Indels 3
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US-10-150-762-6
; Sequence 6, Application US/10150762
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ORGANISM: Artificial Sequence
                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 84.34
Matches 102; Conservative
                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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US-10-013-173-6
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  SEQ ID NO 39
LENGTH: 121
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Sequence 9, Application No. US20050118183A1
GENERAL INFORMATION:
APPLICAMY: ImmunoGen, Inc.
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REFERENCE: A427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT FILING DATE: 2003-11-05
RRIOR APPLICATION NUMBER: US 60/424,332
PRIOR APPLICATION NUMBER: US 60/424,332
SPRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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PUBLICATION NO. US20030219433A1

GENERAL INFORMATION:

APPLICANT: HANSEN, HANS

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: 18733/115

CURRENT APPLICATION NUMBER: US/10/366,709

CURRENT PILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 55

NUMBER OF SEQ ID NOS: 55
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                                                                                                                    Query Match 99.4%; Score 618; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.8e-48;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.6%; Score 613; DB 5; Best Local Similarity 98.3%; Pred. No. 5.1e-48; Matches 116; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73
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US-10-366-709-39
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APPLICANT: HANNA, NABLE,
APPLICANT: HANNA, NABLL
APPLICANT: HEONARD, JOHN E.
APPLICANT: HEONARD, JOHN E.
APPLICANT: NEWANA, KOLAND A.
APPLICANT: REFF, MITCHELL B.
APPLICANT: REFF, MITCHELL B.
APPLICANT: REFF, MITCHELL B.
APPLICANT: RASTETTER, WILLIAM H.
ITITLE OF INVENTION: THERAPERTIC APPLICATION OF CHIMERIC AND RADIOLABELED
ITITLE OF INVENTION: LYMPHONA, BYTIGGN FOR TREATMENT OP B CELL
ITITLE OF INVENTION: LYMPHONA,
ITILE REFERENCE: 37003/0291808
CURRENT FILING DAPE: 2002-09-11
CURRENT FILING DAPE: 1997-08-29
RIOR APPLICATION NUMBER: 08/921,060
RROR FILING DATE: 1993-11-03
PRIOR FILING DATE: 1993-11-03
PRIOR PLING DATE: 1993-11-13
PRIOR PLING DATE: 1992-11-13
                                                                                                                                   NQKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGAGTTVTV 116
                                                          188 NQK-FKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTV 246
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                                  QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                                                                                                                                                                                                                                                                                                                                                         US-10-238-681-11
; Sequence 11, Application US/10238681
; Publication No. US20030147885A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies, Inc. APPLICANT: DeFrees, Shawn APPLICANT: Zopf, David APPLICANT: Bayer, Robert APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANDERSON, DARRELL R. APPLICANT: HANNA, NABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
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| SS 248
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US-10-411-037-62
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LENGTH: 140
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain OTHER INFORMATION: antibody-genomic streptavidin fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                                                             APPLICANT: Schultz, Joanne E. APPLICANT: Lin, Yukang APPLICANT: Lin, Yukang APPLICANT: Lin, Yukang APPLICANT: Lin, Yukang APPLICANT: Banderson, James A.; APPLICANT: Reno, John M. APPLICANT: Dearstyne, Erica A.; TITLE OF INVENTION: STREPTAVILIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF; TILE REFERENCE: 690022.547C2
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.9%; Score 534.5; DB 4; Length 412; 85.2%; Pred. No. 2.6e-40; Live 6; Mismatches 7; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Grahem. Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Sanderson, James Allen
APPLICANT: Bearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED
FILE REFERENCE: 690022.647.
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.9%; Score 534.5; DB 4; Length 412; 85.2%; Pred. No. 2.6e-40; tive 6; Mismatches 7; Indels 5
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Publication No. US20030143233A1
GENERAL INFORMATION:
Publication No. US20030103948A1
GENERAL INFORMATION:
                                                     APPLICANT: Goshorn, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                Graves, Scott S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.9
Best Local Similarity 85.2
Matches 104; Conservative
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Best Local Similarity 85.2
Matches 104; Conservative
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                                                                                APPLICANT:
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publication No. US20040077836A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Begees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Bobert
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GENOUTGATION OF G-CSF
TITLE OF INVENTION: GENOUTGATION OF G-CSF
TITLE OF INVENTION: GOVOUTGATION OF G-CSF
TITLE OF INVENTION: GOVOUTGATION OF G-CSF
TITLE OF INVENTION UNMER: US 60/328,523
FRIOR PELICATION NUMBER: US 60/328,523
FRIOR PELICATION NUMBER: US 60/344,692
FRIOR PELICATION NUMBER: US 60/344,692
FRIOR PELICATION NUMBER: US 60/387,292
FRIOR PELICATION NUMBER: US 60/387,292
FRIOR PELICATION NUMBER: US 60/391,777
FRIOR PELICATION NUMBER: US 60/391,777
FRIOR PELICATION NUMBER: US 60/396,594
FRIOR PELICATION NUMBER: US 60/404,249
FRIOR PELICATION NUMBER: US 60/407,527
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Pred. No. 1e-40;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.8%; Score 533.5; DB 4; Best Local Similarity 83.5%; Pred. No. 1e-40; Matches 101; Conservative 8; Mismatches 9;
                                                           60/407,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 62, Application US/10410962; Publication No. US20040077836A1
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 140
TYPE: PRI
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Best Local Similarity 83.5%;
Matches 101; Conservative
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US-10-410-962-62
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus US-10-411-026-62
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| Sequence 62, Application US/10411026
| Publication No. US20040063911A1
| GENERAL INPORMATION:
| APPLICANT: Neose Technologies, Inc.
| APPLICANT: DeFrees, Shawn
| APPLICANT: DeFrees, Shawn
| APPLICANT: DeFrees, David
| APPLICANT: Chen, Xi
| TITLE OF INVENTION: METHODS
| TITLE OF INVENTION: METHOD OF OR OF OF OR OF OF OR OF OR
                   APPLICANY: CORP., A.A.
APPLICANY: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: ALPHA GALACTOSIDASE A;
TITLE OF INVENTION: ALPHA GALACTOSIDASE A;
FILE REFERENCE: 040853-01-5082
CURRENT FILING DATE: 2003-04-09
PRIOR PELICATION NUMBER: US 60/244, 692
PRIOR PELICATION NUMBER: US 60/344, 692
PRIOR PELICATION NUMBER: US 60/344, 692
PRIOR PELICATION NUMBER: US 60/344, 692
PRIOR PELICATION NUMBER: US 60/341, 777
PRIOR PELICATION NUMBER: US 60/391, 777
PRIOR PELICATION NUMBER: US 60/396, 594
PRIOR PELICATION NUMBER: US 60/404, 249
PRIOR PELICATION NUMBER: US 60/404, 249
PRIOR PELICATION NUMBER: US 60/407, 527
PRIOR APPLICATION NUMBER: US 60/407, 527
PRIOR APPLICATION NUMBER: US 60/407, 527
PRIOR APPLICATION NUMBER: US 60/407, 527
PRIOR PELICATION NUMBER: US 60/407, 527
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APPLICATION NUMBER: US 60/404,249
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APPLICANT: Neces Technologies, Inc.
APPLICANT: DeFrees Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, David
APPLICANT: Bayer, Caryn
TITLE OF INVENTION: BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA: US/10/410,930
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/324,692
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2002-0-0-0
PRIOR PLING DATE: 2002-0-0-0
PRIOR FILING DATE: 2002-0-0-0
PRIOR FILING DATE: 2002-0-0-17
PRIOR FILING DATE: 2002-0-0-17
PRIOR FILING DATE: 2002-0-17
PRIOR PLING DATE: 2002-0-17
PRIOR PLING DATE: 2002-0-16
PRIOR PLING DATE: 2002-0-16
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PRIOR PLING DATE: 2002-0-16
PRIOR PRIOR PLING DATE: 2002-0-16
PRIOR PLING DATE: 2002-0-16
PRIOR PRIOR PLING DATE: 2002-0-16
         APPLICANT: Kazuhisa ULILALA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Mitsuo SATCH
APPLICANT: RYOSUKe NAKANO
ITITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
FILE REPERENCE: 249-289
CURRENT PELLING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: UP 2001-392753
PRIOR APPLICATION NUMBER: UP 2002-106948
PRIOR APPLICATION NUMBER: UP 2002-106948
PRIOR APPLICATION NUMBER: UP 2002-106996
PRIOR APPLICATION NUMBER: UP 2002-11091
PRIOR APPLICATION NUMBER: UP 2002-319975
PRIOR APPLICATION NUMBER: UP 2002-319975
SOFTWARE: PatentIn Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.8%;
Best Local Similarity 83.5%;
Matches 101; Conservative
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Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Howe, Caryn
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
                                                                                            80 NQKFKGKATLTADKSSSTAYMOLSSLTSEDSAVYYCARSTYYGGDWYFNVMGAGTTVTVS 139
                                                          61 NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
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85.8%; Score 533.5; DB 4; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-40;
Matches 101; Conservative 8; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR PILING DATE: 2003-04-09
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/397,292
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
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SECTION 06: 75
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Sequence 14, Application US/10327663

Publication No. US20040093621A1

FRIBRAL INFORMATION:
APPLICANT: Kenya SHITARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Mus musculus
US-10-411-049-62
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US-10-410-997-62
PUBLICARION NO. US20040126838A1
GENERAL HUNCARATION:
APPLICANT: Decreas, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bayer
CHOR PRINCE Caryon
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCCONJUGATION OF
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCCONJUGATION OF
FILE REPRENCE: 040853-01-509
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT APPLICATION NUMBER: US 60/328,523
FRIOR FILING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PELING DATE: 2002-08-16
PRIOR PELING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PELING DATE: 2002-08-16
PRIOR PELING DATE: 200
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85.8%; Score 533.5; DB 4; Length 140;

Best Local Similarity 83.5%; Pred. No. 1e-40;

Matches 101; Conservative 8; Mismatches 9; Indels 3
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Wus musculus
US-10-410-930-62
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US-10-410-997-62
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Scoring table:

Searched:

Perfect score:

Sequence:

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Sequence 30, Appl
Sequence 31, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 123, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 7, Appl
Sequence 7, Appl
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Sequence 7, Appl
Sequence 12, Appl
Sequence 201, Appl
Sequence 31, Appl
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| Sequence 35, Application US/11107028
| Sequence 35, Application US/11107028
| Publication No. US20050276803A1
| GENERAL INFORMATION:
| APPLICANT: CHAN, ANDREW C.
| APPLICANT: GONG, QIAN
| APPLICANT: GONG, QIAN
| APPLICANT: MARTIN, FLAVIUS
| TITLE OF INVENTION: Method for Augmenting B Cell Depletion
| FILE REFERENCE: P2112R1
| CURRENT FILING DATE: 2005-04-15
| PRIOR PILING DATE: 2004-04-16
| NUMBER OF SEQ ID NOS: 52
| SEQ ID NO 35
| LENGTH: 121
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9 US-10-662-36

9 US-10-649-866-19

11 US-11-054-669-123

12 US-10-507-662-32

13 US-11-07-028-38

9 US-10-507-662-35

10 US-11-297-317-4

10 US-11-297-317-4

9 US-10-932-334-7

9 US-10-932-334-7

9 US-10-932-334-7

9 US-10-932-334-7

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10 US-11-07-088-11

11 US-11-107-088-11
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US-11-226-325-201
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US-11-226-325-4
US-11-097-812-31
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84.3%; Pred. No. 3.4e
:ive 6; Mismatches
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US-11-183-218-62
; Sequence 62, Application US/11183218
; Publication No. US20060088906A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
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Best Local Similarity 84.3
Matches 102; Conservative
     788.8
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score greater than or equal to the score of the result being printed,
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Sequence 20, 7
Sequence 18, Sequence 18, Sequence 20, 3
Sequence 21, Sequence 31, Sequence 
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Sequence 5,
Sequence 7,
Sequence 25,
Sequence 25,
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622
1 QVQLQQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTTVTVSS
                                                                                                                                                                                                  May 9, 2006, 01:59:22; Search time 14.0476 Seconds
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| SIDS5/ptodata/2/pubpaa/USOB_NEW_PUB.pep1:*
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and is derived by analysis of the total score distribution.
                                GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-183-218-62
US-11-184-620-5
US-11-124-620-7
US-11-254-182-28
US-11-26-318-7
US-11-106-820-7
US-11-106-820-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-147-780-18
US-11-147-780-18
US-11-107-028-27
US-11-107-028-37
US-11-107-028-37
US-11-107-028-37
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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9

Gaps

Score

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CURRENT APPLICATION NUMBER: US/11/183,205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 533.5; DB 10; Length 140;
Pred. No. 6.9e-38;
8; Mismatches 9; Indels 3;
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APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-US01
                                                                                                                       APPLICANT: 20Pt. David
APPLICANT: APPLICANT: ADVIG
APPLICANT: APER, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/11183205
Publication No. US20060030521A1
GENERAL INFORMATION:
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
                                         APPLICANT: Neose Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.5%;
Matches 101; Conservative
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Zopf, David
Bayer, Robert
Bowe, Caryn
Hakes, David
Chen, Xi
                                                                   DeFrees, Shawn
Zopf, David
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US-11-183-218-62
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61 NOKFKGKATLIADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
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CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 11/183, 205
PRIOR PILING DATE: 2005-07-15
PRIOR PILING DATE: 2005-07-15
PRIOR PILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR PILING DATE: 2001-07
PRIOR APPLICATION NUMBER: US 60/387, 292
PRIOR APPLICATION NUMBER: US 60/387, 292
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/407, 527
PRIOR PILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
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CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: US 60/568,440
PRIOR PILING DATE: 2004-07-15
PRIOR PELING DATE: 2004-07-15
PRIOR PELING DATE: 2004-07-20
PRIOR PELING DATE: 2004-07-20
PRIOR PELING DATE: 2004-11-09
PRIOR PILING DATE: 2004-11-09
PRIOR PILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR PILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
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APPLICANT: Dang, Wei
APPLICANT: Desjarlais, John R.
APPLICANT: Rarki, Sher Bahadur
APPLICANT: Vafa, Omid
APPLICANT: Nafa, Omid
APPLICANT: TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/11124620 Publication No. US20060024298A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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CRGANISM: Mus musculus
US-11-183-205-62
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Best Local Similarity
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APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE REFERENCE: P2158R1
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Pred. No. 1.9e-37;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/11208422 Publication No. US20060067930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                          ; Sequence 7, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin version 3.3 SEQ ID NO 7 LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 83.5%;
Similarity 83.5%;
11; Conservative
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US-11-124-620-7
                 118 S 118
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Best Local Simi
Matches 101;
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LOCATION: (335). (335). (335)
OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine
OTHER INFORMATION: or Glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (243)...(243)...(243)
OTHER INPORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
OTHER INFORMATION: Glutamine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 120
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LOCATION: (244)
LOCATION: (244)
LOCATION: (244)
LOCATION: (245)
LOCATION: (268)
LOCATIO
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OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid
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LOCATION: (334)..(334)
OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
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LOCATION: (330)..(330)
OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine
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LOCATION: (3027..(302)
OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (301)...(301)
OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (276)..(276)
OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (278)..(278)
OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
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GENERAL INFORMATION:
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85.8%; Score 533.5; DB 11; Length 451;
Best Local Similarity 83.5%; Pred. No. 1.9e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3;
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US-11-254-182-28
Sequence 28, Application US/11254182
Publication No. US20060088523A1
GENERAL INFORMATION:
APPLICANT: ANDYA, JAMES
APPLICANT: GWEE, SHIANG C.
APPLICANT: LIU, JUN
FILE OF INVENTION: ANTIBODY FORMULATIONS
FILE REFERENCE: P2104R1
CURRENT PAPLICATION NUMBER: US/11/254,182
CURRENT FILING DATE: 2005-10-19
PRIOR APPLICATION NUMBER: US 60/620,413
PRIOR APPLICATION NUMBER: US 620,413
PRIOR PILING DATE: 2004-10-20
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 28
LENGTH: 122
TAPE: NUMBER OF SEQ ID NOS: 74
TAPE: NUMBER OF SEQ ID NOS: 77
                                                                                                                                                                                                ; OTHER INFORMATION: sequence is synthesized US-11-208-422-25
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
LENGTH: 451
                                                                                                                                                             ORGANISM: Artificial sequence
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US-11-254-182-28
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121 A 121
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; Sequence 7, Application US/11120338 ; Publication No. US20050271658A1

US-11-120-338-7

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61 NQKFKGKATLITVDKSSSTAYMQLSSLTSEDSAVYFCARVVYSNSYMYFDVWGTGTIVIV 120
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APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IOBAL S.
APPLICANT: WALLCKE, PATERCIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE FILE REFRENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT PILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-05
PRIOR FILING DATE: 2004-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/11106820
Publication No. US2006002930A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G
APPLICANT: BEWELL, KATHRYN L.
TITLE OF INVENTION: Treatment of Disorders
FILE REFERENCE: P2102A1
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US/11/106,820
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/563,227
PRIOR APPLICATION NUMBER: US 60/563,098
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/565,098
PRIOR FILING DATE: 2004-04-16
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Best Local Similarity 79.55
Matches 97; Conservative
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SEQ ID NO 7
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61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTV 120
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JAPPLICANT: Adams ET AL.
JITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
JETLE REPRENCE: P1990R3C1
CURRENT APPLICATION NUMBER: US/11/147,780
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US 60/434,115
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2003-12-01
PRIOR FILING DATE: 2003-12-01
PRIOR FILING DATE: 2003-12-01
PRIOR FILING DATE: 2003-12-01
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 507; DB 11; Length 122;
Pred. No. 9.8e-36;
7; Mismatches 14; Indels
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Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHMA.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
FILE REPRENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT ELLING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/576,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
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Pred. No. 9.8e-36;
7; Mismatches 14;
                                                                                                                                                                                                         Sequence 7, Application US/11147780; Publication No. US20060034835A1; GENERAL INFORMATION:
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79.5%;
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NUMBER OF SEQ ID NOS: 25
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 79.5
Matches 97; Conservative
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Best Local Similarity
Matches 97; Conserva
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121 SS 122
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ITLEO FOR INVENTION: Immunoglobulin Variants and Uses Thereof FILE REFERENCE: P1990R3CIP1)
CURRENT APPLICATION NUMBER: US/11/190,364
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: US 60/434,115
PRIOR APPLICATION NUMBER: US 60/526,163
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR APPLICATION NUMBER: US 11/147,780
PRIOR PILING DATE: 2003-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels
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Pred. No. 9.8e-36;
7; Mismatches 14; Indels
                          Sequence 7, Application US/11143077

Publication No. US20060024295A1

GENERAL INFORMATION:

APPLICANT: Brunetta, Paul G.

TITLE REFERENCE: P2133R1

CURRENT FILING DATE: 2005-06-02

PRIOR APPLICATION NUMBER: US/11/143,077

CURRENT FILING DATE: 2004-06-04

PRIOR FILING DATE: 2004-06-11

RIOR FILING DATE: 2004-10-11

NUMBER OF SEQ ID NOS: 24
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Publication No. US20060024300A1
GENERAL INFORMATION:
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Best Local Similarity 79.55
Matches 97; Conservative
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US-11-143-077-7
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NOKFKGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGAGTTVTV 116
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81.5%; Score 507; DB 11; Length 253;
Best Local Similarity 79.5%; Pred. No. 1.9e-35;
Matches 97; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                               RESULT 14
US-11-187-364-7
; Sequence 7, Application US/11187364
; Publication No. US20060062781A1
; GENERAL INFORMATION:
; AFPLICANT: Hitraya, Elena
; TITLE OF INVENTION: WETHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR PILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 7
; LENGTH: 122
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81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels
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| Sequence 20, Application US/11106820
| Sequence 20, Application US/11106820
| Publication No. US20060002930A1
| GENERAL INFORMATION:
| APPLICANT: BRUNETTA, PAUL G
| APPLICANT: BENELL, KATHKNY L.
| TTILL OF INVERTION: Treatment of Disorders
| FILE REFERENCE: P2102R1
| CURRENT APPLICATION UNMBER: US/11/106,820
| CURRENT FILING DATE: 2005-04-15
| PRIOR FILING DATE: 2004-04-16
| PRIOR FILING DATE: 2004-04-15
| SEQ ID NO 20
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ORGANISM: Artificial sequence
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; ORGANISM: Mus musculus
US-11-187-364-7
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9
                      24 QAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY
QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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Job time : 15.0476 secs
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May 9, 2006, 01:18:21; Search time 101.749 Seconds (without alignments) 487.964 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	lon	Mouse ant	Mouse ant	Murine SM	Mouse ant	Mouse SM5	Novel chi	SMS-1 chi	Novel chi	FL/Fc/chS	Novel chi	S. aureus	Antibody	Murine an	Humanized	S. aureus	Humanised	HEV relat	MAb 022 V	S. aureus	Synthetic	Binding d	Synthetic	Mouse G28	Mouse ant
	Description	Ado32092	Ado32146	Adx37184	Aea88701	Adv92466	Adv98529	Adv92470	Adv98533	Adv92490	Adv98553	Aae29266	Adu39970	Aea38741	Aea38768	Aae29264	Ado32094	Adb97820	Aar54933	Aae29268	Abg31024	Add25453	Adm42728	Aeb95396	Aeb94430
SUMMARIES		1092	146	184	1701	466	1529	470	1533	490	1553	1266	970	1741	1768	1264	.094	820	.933	1268	.024	453	728	396	430
SO	a	AD032092	AD032146	ADX37184	AEA8870	ADV92466	ADV98529	ADV9247	ADV98533	ADV92490	ADV98553	AAE29266	ADU39970	AEA38741	AEA38768	AAE29264	AD032094	ADB97820	AAR54933	AAE29268	ABG31024	ADD25453	ADM42728	AEB95396	AEB94430
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	Length	113	114	113	113	133	133	239	239	661	661	112	112	116	667	112	113	113	112	112	272	272	272	272	272
•	* Query Match	100.0	100.0	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.6	93.6	93.6	93.6	93.5	93.5	93.1	92.8	92.1	91.9	91.9	91.9	91.9	91.9
	Score	581	581	545	545	545	545	545	545	545	545	544	544	544	544	543	543	541	539	535	534	534	534	534	534
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527 527 527 527 527 528 528 528 528 520 520 520 520 520 520 520 520 520 520	2092 8 2092; JG-200 = anti -CD33 lement cody; nic my nic my nic my nic my nic my	IMB MG,
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composition comprising the immunoconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD13; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment to polymucleotide encoding the antibody or its epitope-binding fragment to contain a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment to contain antibody or its epitope-binding fragment to contain antibody defined above or its epitope-binding fragment to comprising the polymucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD3; and (13) cobtaining CD3; from a biological material. The anti-CD3 antibody has cytostatic activity. The antibody or its epitope-binding fragment, composition can be used for treating copiect having a cisease where CD3; is expressed such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. CT can also be used for inhibiting the growth of cells expressing CD3; and for in vivo imaging or as affinity purification agents. The present sequence represents the mouse anti-CD3 antibody My9-6 light chain. ö New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60 1 NIMLTQSPSSLAVSAGEKVTWSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60 anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodyaplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain. Gaps Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62. 61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113 ö Query Match 100.0%; Score 581; DB 8; Length 113; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 113; Conservative 0; Mismatches 0; Indels ( AD032146 standard; protein; 114 AA Lutz RJ; 05-NOV-2003; 2003WO-US032737. 07-NOV-2002; 2002US-0424332P. (first entry) Tavares D, (IMMU-) IMMUNOGEN INC WPI; 2004-411619/38. Sequence 113 AA; WO2004043344-A2. Mus musculus. 12-AUG-2004 27-MAY-2004 Hoffee MG, AD032146; RESULT 2 ADO32146 888888888888888888888888888888888 음 Š ठ

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The present invention describes an isolated anti-UJ3 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region. Comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD3. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the antibody or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the immunoconjugate, composition or the antibody or antibody fragment is labelled; (5) inhibiting the agent, where the antibody or antibody fragment is labelled; (5) inhibiting the cell agent of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment; (10) an isolated polymucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment that specifically binds to CD33; (8) an isolated bolymucleotide encoding a light or heavy chain of the antibody or its epitope-binding fragment; (10) an isolated bolymucleotide encoding a subject having a recombinant vector comprising the polymucleotide encoding a subject having a cycostatic activity. The antibody or its epitope-binding fragment having the ability to bind CD33; and composition can be used for treating a subject having a disease where CD31 is expressed, such as myeloid leukaemia, chronic myeloid leukaemia or processing CD3 antibody or its epitope-binding fragment a more constinant as a sequence represents a mouse anti-cD33 antibody or sequence, which is used in an example from the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine SM5-1 antibody, mSM5-1, light chain variable region, SEQ ID 4.
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                                                                                         present invention describes an isolated anti-CD33 antibody
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100.0%; Pred. No. 1.7e-39;
tive 0; Mismatches 0;
                                              Example 3; SEQ ID NO 62; 124pp; English.
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or chronic myeloid leukemia.
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vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Mature Mouse SMS-1 (mSMS-1) light chain variable region protein"
                                                                                                                                                                           New antibody competitively inhibiting immunospecific binding of a human SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful in treating malignancies such as melanoma, breast cancer or hepatocellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody engineering; chimeric antibody; cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%; Score 545; DB 9;
92.0%; Pred. No. 1.3e-36;
ive 5; Mismatches 4;
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                                                  (SYMB-) SYMBIGENE ACQUISITION CO INC.
                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 4; 85pp; English.
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26-NOV-2003; 2003US-00722849.
28-NOV-2003; 2003TW-00133571.
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25-NOV-2003; 2003CN-01119930.
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Matches 104; Conservative
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                                                                                                                      WPI; 2005-435284/44.
N-PSDB; AEA88705.
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                                                                                      Gno X;
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                                                                                                                                                                                                                                      carcinoma
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                                                                                                                                                                                                                                                                                                                                        The present invention relates to antibodies which are specific for the cancer associated antigen SMS-1. The antibodies are useful for assaying for SMS-1 antigen in a sample, which is useful for the prognosis or diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma. The present sequence is a variable region of one such anti-SMS
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:e= "Variable region"
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/note= "Variable region"
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                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 4; 40pp; English.
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             06-JUN-2003; 2003CN-00129123
25-NOV-2003; 2003CN-01119926
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25-NOV-2003; 2003CN-01119926.
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Matches 104; Conservative
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                                                                  MA J.
GUO Y.
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                                                                (MAJJ/) (GUOY/)
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Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
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25-NOV-2003; 2003CN-01119930.
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92.0%;
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Best Local Similarity 92.0°
Matches 104; Conservative
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                                                                                                                                                                                                                                                 of the invention.
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(GUOY/) GUO Y.
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Chimeric.
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                         agent.
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                                                                                                                                                                                                                                                                                                           The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the mouse SMS-1 (mSMS-1) light chain variable region protein.
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                                                                                                                                                                                New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel chimeric protein-related mSM5-1 light chain protein SeqID10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%; Score 545; DB 9; Length 133; 92.0%; Pred. No. 1.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein engineering; pharmaceutical; cytostatic; vaccine; c
neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 10; 158pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-2003; 2003CN-00129290.
25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
28-NOV-2003; 2003TW-00133577.
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Matches 104; Conservative
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N-PSDB; ADV98528.
                                                                                                                      WPI; 2005-030218/03.
                                                                                                                                              N-PSDB; ADV92465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 133 AA;
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                   (MAJJ/) MA J.
(GUOY/) GUO Y.
                                                                                 Guo Y;
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                                                                                    Ма J,
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                                                          This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 545; DB 9; Length 133;
Pred. No. 1.6e-36;
5; Mismatches 4; Indel8

    133
    'note= "Light chain variable region gene"

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Example 3; SEQ ID NO 10; 147pp; English
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/label= Signal peptide
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ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, as melanoma, breast cancer or hepatocellular carcinoma. The present equence is that of a protein which is related to the chimeric proteins of the invention. Note: Two sequences were allocated this SeqID number in the specification, the alternative sequence is shown on page 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                              NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 80
                                                                                                                                                                                                                                                                           1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region gene (VH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Light chain variable region gene (VL)"
                                                                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature FL/Fc/chSMFv fusion protein"
                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                     Score 545; DB 9;
Pred. No. 2.7e-36;
                                                                                                                                                                                                                                       5; Mismatches
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/label= Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "CH2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308. .414
/note= "CH3 region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV92490 standard; protein; 661 AA
                                                                                                                                                                                                  93.8%;
92.0%;
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25-NOV-2003; 2003CN-01119930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FL/Fc/chSMFv fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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534. .5
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                                                                                                                                                                                                                      Similarity
                                                                                                                                                                  Sequence 239 AA;
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Chimeric.
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                                                                                                                                                                                                     Query Match
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Peptide
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                                                                                                                                           The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the SMS-1 chimeric antibody (ChSM) light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                      21 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 80
                                   New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
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Pred. No. 2.7e-36;
5; Mismatches 4; Indels
                                                                                                         Example 3; SEQ ID NO 14; 158pp; English
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2003US-00723003.
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Matches 104, Conservative
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N-PSDB; ADV98532.
   N-PSDB; ADV92469
                                                                                                                                                                                                                                                                                          Sequence 239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-2003;
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This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, such
                                                                                                                                                                                                 as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein; immunological; staphylococcal infection; impetigo; pneumonia; furuncle septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                        549 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                  1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti- clumping factor A (ClfA) monoclonal antibody, useful for treating or preventing Staphylococcus aureus infection e.g. wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.
                                                                                                                                                                                                                                                                                                                              93.8%; Score 545; DB 9; Length 661; 92.0%; Pred. No. 7.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7.2e
5; Mismatches
                                                          Claim 23; SEQ ID NO 34; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ъ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29266 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domanski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24. .40
/note= "CDR1"
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/note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95. .102
/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-2001; 2001US-0264072P.
12-MAR-2001; 2001US-0274611P.
18-JUL-2001; 2001US-0229413P.
30-JUL-2001; 2001US-0308116P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2002; 2002WO-US002296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patti JM, Hutchins JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INHI-) INHIBITEX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-759834/82.
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD46865.
                                                                                                                                                                                                                                                                                          Sequence 661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200272600-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                   The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the FL/FC/chSMFv fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                             New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYMASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 BSGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 545; DB 9; Length 661; 92.0%; Pred. No. 7.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                              Claim 23; SEQ ID NO 34; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYMB-) SYMBIGENE ACQUISITION CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADV98553 standard; protein; 661 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-2004; 2004WO-US017765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2003; 2003CN-00129290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 104; Conservative
                                                                                                WPI; 2005-030218/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-075540/08.
N-PSDB; ADV98552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 661 AA;
                                                                                                                        N-PSDB; ADV92489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005001048-A2.
(GUOY/) MA J. (GUOY/) GUO Y.
                                                            Guo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma J, Guo Y;
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Synthetic.
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furuncle;

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The invention relates to an isolated antibody capable of binding to human
                                               Sequence 112 AA;
                                                                                                                                   WO2004094475-A2
                                                                                                                             sapiens
                                                                                                          27-JAN-2005
                                                                                                                                        04-NOV-2004
                                                                                                    ADU39970;
                                                                                                                                                                                              such as
                                                                                                                                                                 (WANG/)
                                                                                                                                                                       Wang B;
                                                                                                                             Homo
                                                                                         RESULT 12
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ö The invention relates to monoclonal antibody which binds the clumping factor A (CIfA) protein from Staphylococcus aureus. The anti-clfA monoclonal antibody is useful for treating or preventing S. aureus infection in a human or animal, and for inhibiting the binding of staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment S. aureus CIfA) protein, or the S. aureus N3 protein is useful for inducing an immunological response in a human or animal. These staphylococcal infections include wound infections, sepsis, impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The present sequence is Staphylococcus aureus CIfA specific monoclonal antibody 12-9VLA-1 (variable light sequence) protein infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in 9 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFPSSSQKNYLAWYQQIPGQSPKLLIYWASTR New antibodies capable of binding to human tissue factor and do not inhibit tissue factor mediated blood coagulation compared to a normal plasma control, useful for diagnosing, preventing or treating cancer, Gaps cytostatic; gene therapy; human tissue factor; antibody engineering; blood; coagulation; plasma; diagnosing; cancer. ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIK 112 ö Length 112; Score 544; DB 5; Length 11 Pred. No. 1.6e-36; 5; Mismatches 3; Indels Antibody TF9 light chain variable region. Disclosure; SEQ ID NO 31; 134pp; English Claim 11; Page 35; 80pp; English. ADU39970 standard; protein; 112 22-APR-2003; 2003US-0464363P. 26-JUN-2003; 2003US-0482498P. 05-APR-2004; 2004US-00816938. 93.6%; 92.9%; 21-APR-2004; 2004WO-US012206 (first entry) Best Local Similarity 92.9 Matches 104; Conservative (EURO-) EUROCELTIQUE SA. (WANG/) WANG B. breast cancer. WPI; 2004-795533/78. N-PSDB; ADU39969. human or animal

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tissue factor (TF), which does not inhibit tissue factor mediated blood coagulation compared to a normal plasma control and can initiate an Fc-mediated mechanism. The composition and methods are useful for diagnosing, preventing or treating cancer, such as non-small cell lung cancer, breast cancer, colon cancer or prostate cancer. These may also be used in screening for agents that may treat or prevent cancer. This sequence corresponds to the light chain variable region of an anti-human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening compounds useful for treating tumor metastasis involves administering a test compound to non-human animal model bearing soft tissue/bone metastasis and identifying compound that inhibits soft tissue growth/bone metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; animal disease model; metastasis; cytostatic; copplasm; bone metastases; breast tumor; colorectal tumor; bone disease; osteopathic; antibody therapy; radiation therapy; immunotherapy; cancer cell proliferation inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transforming growth factor-beta-antagonist; light chain variable region.
                                                                                                                                                                                                                                                     1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPQQSPKLLIYWASTR
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                                                                                                                                                                                                                                     1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - L2"
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the screening of candidate molecules
                                                                                                                                                                                                                                                                                                  ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                    ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complementarity determining region (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CDR)
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.
                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complementarity determining region
                                                                                                                                                                                                        3; Indels
                                                                                                                                                                        Score 544; DB 8;
Pred. No. 1.6e-36;
5; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           AEA38741 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003; 2003US-0520398P. 31-MAR-2004; 2004US-0557951P.
                                                                                                                                                                           93.6%;
92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                               Query Match
Best Local Similarity 92.9
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95..10
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                                                                                                             tissue factor antibody
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                                                                                                                                            Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005050200-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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of tumor metastasis and treatment methods using such molecules. The screening method of the invention involves administering several test substances to a non-human syngeneic immunocompetent animal model bearing to the livest tissue or bone metastasis optionally in presence of a primary tumor, determining the effects of these test substances on the primary tumor, determining the effects of the primary tumor and identifying a test substance inhibiting soft tissue growth or bone metastasis without adverse effect on the status of the primary tumor. The invention is useful in the diagnosis and treatment of breast cancer, cloractal cancer, liver and lung metastases, bone destruction and bone loss. The animal models of the present invention is useful to screen substances useful for the prophylaxis or treatment of soft tissue and/or bone metastases which may additionally be effective in treating the primary tumor. The present sequence is murine anti-TGF-beta antibody carriant with the prophylaxis and treatment of soft tissue and/or brimary tumor. The present sequence is murine anti-TGF-beta antibody protein. anti-transforming growth factor (TGF)-beta antibodies] for the treatment Length 116; Query Match 93.6%; Score 544; DB 9; Best Local Similarity 92.0%; Pred. No. 1.7e-36; Matches 104; Conservative 6; Mismatches 3; Sequence 116 AA; \$

ö 9 1 DIMMIQSPSSLAVSAGEKVIMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR Gaps ; 3; Indels 8

61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR ò 원

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RESULT 14 **AEA38768** 

Ä AEA38768 standard; protein; 667

AEA38768;

11-AUG-2005 (first entry)

Humanized murine anti-TGF-beta antibody protein, chimL.chimH, SEQ: 28.

Monoclonal antibody; animal disease model; metastasis; cytostatic; neoplasm; bone metastasses; breast tumor; colorectal tumor; bone disease; osteopathic; antibody therapy; radiation therapy; immunotherapy; cancer cell proliferation inhibitor; transforming growth factor-beta-antagonist; humanized antibody; chimeric antibody. 

musculus. Mus

Homo sapiens. Synthetic.

Chimeric

Location/Qualifiers /label= Unknown Misc-difference

WO2005050200-A2

02-JUN-2005

04-NOV-2004; 2004WO-US036651

13-NOV-2003; 2003US-0520398P. 31-MAR-2004; 2004US-0557951P.

(GETH ) GENENTECH INC

Filvaroff

WPI; 2005-417772/42.

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[anti-transforming growth factor (TGP)-beta antibodies] for the treatment of tumor metastasis and treatment methods using such molecules. The screening method of the invention involves administering several test substances to a non-luman syngemeic immunocompetent animal model bearing at least one soft tissue or bone metastasis optionally in presence of a primary tumor, determining the effects of these test substances on the soft tissue or bone metastasis and growth of the primary tumor and identifying a test substance inhibiting soft tissue growth or bone metastasis without adverse effect on the status of the primary tumor. The invention is useful in the diagnosis and treatment of breast cancer, colorectal cancer, liver and lung metastasis, on the growth or and bone colorectal cancer, liver and lung metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      loss. The animal models of the present invention is useful to screen substances useful for the prophylaxis or treatment of soft tissue and/or bone metastusses which may additionally be effective in treating the primary tumor. The present sequence is humanized murine anti-transforming growth factor-beta (anti-TGF-beta) antibody (also refered as humanized monoclonal antibody 2G7) chimeric protein.
Screening compounds useful for treating tumor metastasis involves administering a test compound to non-human animal model bearing soft tissue/bone metastasis and identifying compound that inhibits soft tissue growth/bone metastasis.
                                                                                                                                                                                                                             present invention relates to the screening of candidate molecules
                                                                                                                                                                 Example 2; SEQ ID NO 28; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 667 AA;
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Gaps ő 93.6%; Score 544; DB 9; Length 667; 92.0%; Pred. No. 8.7e-36; ive 6; Mismatches 3; Indels Matches 104; Conservative Local Similarity

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RESULT 15 AAE29264

AAE29264 standard; protein; 112 AA

AAE29264;

(first entry) 27-JAN-2003 S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.

furuncle; Clumping factor A, ClfA, fibrinogen; fibrin; Clf40; Clf33; N3 protein; immunological; staphylococcal infection; impetigo; pneumonia; furuncle septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

Staphylococcus aureus.

Location/Qualifiers "CDR1" 24. .40 /note= "( Region

Region

56. .62 /note= "CDR2" .e= .102 - "CDR3" Region

WO200272600-A2

19-SEP-2002.

28-JAN-2002; 2002WO-US002296 

26-JAN-2001; 2001US-0264072P. 12-MAR-2001; 2001US-0274611P.

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New anti- clumping factor A (ClfA) monoclonal antibody, useful for treating or preventing Staphylococcus aureus infection e.g. wound infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in a human or animal.
                                                                                                                                                                                                                                                                                                                                                   The invention relates to monoclonal antibody which binds the clumping factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA monoclonal antibody is useful for treating or preventing S. aureus infection in a human or animal, and for inhibiting the binding of staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment S. aureus ClfA) protein, S. aureus (ClfA) protein, s. aureus (ClfA) protein, or the S. aureus N3 protein is useful for inducing an immunological response in a human or animal. These staphylococcal infections include wound infections, sepsis, impetigo, furunoles, pneumonia, septic arthritis or endocarditis. The antibody 13-2VLA-1 (variable light sequence) protein
                                                                                                      Domanski P, Patel P, Hall A;
                                                                                                                                                                                                                                                                                                                Claim 11; Page 34; 80pp; English.
  18-JUN-2001; 2001US-0298413P. 30-JUL-2001; 2001US-0308116P.
                                                                                                      Patti JM, Hutchins JT,
                                                            (INHI-) INHIBITEX INC
                                                                                                                                               WPI; 2002-759834/82.
                                                                                                                                                                 N-PSDB; AAD46863.
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1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFPSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60 1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPQQSPKLLIYWASTR 60 0; Gaps Query Match 93.5%; Score 543; DB 5; Length 112; Best Local Similarity 92.0%; Pred. No. 1.9e-36; Matches 103; Conservative 6; Mismatches 3; Indels ò 셤 ઠે

Sequence 112 AA;

Search completed: May 9, 2006, 01:25:28 Job time : 101.749 secs

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n 5.1.8
Biocceleration Ltd.
GenCore version
Copyright (c) 1993 - 2006
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OM protein - protein search, using sw model

May 9, 2006, 01:25:51; Search time 17.1212 Seconds (without alignments) 635.031 Million cell updates/sec Run on:

US-10-700-632-8 581 Title: Perfect score:

1 NIMLTQSPSSLAVSAGEKVT......CHQYLSSRTFGGGTKLEIKR 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database :

¥.

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		kappa			kappa		kappa		Ig light chain V r	kappa	light	kappa			kappa chain	kappa chain	kappa			chain	antibody light cha		PL7-6 antibody lig	תח		kappa	Ig kappa chain V r	titumor	kappa	Ig kappa chain V r
B ID		_				2 PS0023		2 S26040	2 PT0407	2 \$09970	2 \$26337	2 PL0265	2 PC1214	2 PL0014	2 S06084	1 K4HUJI	2 A31790	2 S34002	2 PT0408	1 K4HULN	2 S51147	2 PL0263	2 JC2270	2 S49531	-	2 830520	2 \$34003	2 A49260	82	2 830523
Length DB		111	103	112	112	133	118	138	113	112	101	112	134	145	240	133	220	113	113	114	120	113	113	134	135	113	113	113	214	113
* Query Match Length		90.4	85.7	85.4	84.0	84.0	83.8	83.3	82.8	82.3	81.9	81.9	81.5	81.5	81.3	80.7	90.6	79.8	79.7	79.1	78.9	78.7	78.7	78.7	78.7	78.6	78.6		78.2	
Score	1 1 1	525	498	496	488	488	487	484	481	478	476	476	473.5	473.5	472.5	469	468.5	463.5	463	459.5	458.5	457.5	457.5	457.5	457.5	456.5	456.5	455.5	454.5	450.5
Result No.		-	7	e	4	S	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56			29

-	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain
PH1101	F30538	E30538	S26336	S44119	PH1104	A53261	S46373	PH1050	PH1103	PL0264	S44116	S03304	K4HU17	PH1047
7	0	N	N	N	~	N	~	~	0	N	~	0	ч	7
104	112	112	109	114	104	138	132	103	104	113	114	111	134	103
77.1	77.0	6.97	76.7	76.7	9.9/	9.9/	76.3	76.2	76.1	76.0	0.92	75.6	75.5	74.9
448	447.5	446.5	445.5	445.5	445	445	443.5	443	442	441.5	441.5	439.5	438.5	435
31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
	448 77.1 104 2 PH1101 Ig light (	448 77.1 104 2 PH1101 Ig light chain 447.5 77.0 112 2 F30538 Ig kappa chain	448 77.1 104 2 PH1101 IG light chain 447.5 77.0 112 2 P30538 IG kappa chain 146.5 76.9 112 2 R30538 IG kappa chain	448     77.1     104     2     PH1101     Ig light chain       447.5     77.0     112     2     F30538     Ig kappa chain       446.5     76.9     112     2     E30538     Ig kappa chain       445.5     76.7     109     2     S26336     Ight chain	448     77.1     104     2     PH1101     Ig light chain       447.5     77.0     112     2     F30538     Ig kappa chain       446.5     76.9     112     2     830538     Ig light chain       445.5     76.7     119     2     826536     Ig light chain       445.5     76.7     114     2     844119     Ig kappa chain	448     77.1     104     2     PH1101     Ig light chain       447.5     77.0     112     2     P30538     Ig kappa chain       446.5     76.9     112     2     830538     Ig kappa chain       445.5     76.7     109     2     826336     Ig light chain       445.5     76.7     114     2     844119     Ig kappa chain       445     76.6     104     2     PH1104     Ig hight chain	448         77.1         104         2         PH1101         Ig light chain           446.5         77.0         112         2         F30538         Ig kappa chain           446.5         76.9         112         2         F30538         Ig kappa chain           445.5         76.7         109         2         S26336         Ig light chain           445.5         76.6         114         2         S44119         Ig kappa chain           445         76.6         134         2         A511104         Ig kappa chain           445         76.6         138         2         A53261         Ig kappa chain           19         138         2         A53261         Ig kappa chain	448     77.1     104     2     PH1101     Ig light chain       447.5     77.0     112     2     F30538     Ig kappa chain       446.5     76.9     112     2     S26336     Ig kappa chain       445.5     76.7     109     2     S26336     Ig light chain       445.5     76.7     114     2     S44119     Ig kappa chain       445     76.6     104     2     PH1104     Ig kappa chain       445     76.6     138     2     A53251     Ig kappa chain       443.5     76.3     132     2     S46373     Ig kappa chain	448         77.1         104         2         PH1101         Ig light chain           446.5         76.9         112         2         F30538         Ig kappa chain           446.5         76.9         112         2         S26336         Ig kappa chain           445.5         76.7         109         2         S26336         Ig kappa chain           445.5         76.7         114         2         S44119         Ig kappa chain           445         76.6         138         2         A52261         Ig kappa chain           443.5         76.3         132         2         S46373         Ig kappa chain           443.5         76.2         103         2         PH1050         Ig kappa chain           443.5         76.2         193         2         PH1050         Ig kappa chain	448         77.1         104         2         PH1101         Ig light chain           446.5         76.9         112         2         F30538         Ig kappa chain           446.5         76.9         112         2         S26336         Ig kappa chain           445.5         76.7         109         2         S26336         Ig light chain           445.5         76.7         104         2         PH1104         Ig kappa chain           445         76.6         138         2         A53261         Ig kappa chain           443.5         76.3         132         2         S46573         Ig kappa chain           443.5         76.2         103         2         PH11050         Ig light chain           447         76.1         104         2         PH11050         Ig light chain	448         77.1         104         2         PH1101         Ig light chain           446.5         76.9         112         2         F30538         Ig kappa chain           446.5         76.9         112         2836338         Ig kappa chain           445.5         76.7         109         2         S26336         Ig light chain           445.5         76.6         104         2         PH1104         Ig kappa chain           445         76.6         138         2         A53261         Ig kappa chain           443.5         76.2         103         2         PH1050         Ig light chain           443.7         76.2         103         2         PH1050         Ig light chain           443.7         76.2         103         2         PH1050         Ig light chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         113         2         PL0264         Ig kappa chain	448         77.1         104         2         PH1101         Ig light chain           446.5         76.9         112         2         F30538         Ig kappa chain           446.5         76.9         112         2         S26336         Ig kappa chain           445.5         76.7         109         2         S26336         Ig kappa chain           445.5         76.7         104         2         PH1104         Ig kappa chain           445         76.6         138         2         A52361         Ig kappa chain           443.5         76.3         132         2         S46373         Ig kappa chain           443.5         76.0         104         2         PH1050         Ig kappa chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         114         2         PL1064         Ig kappa chain	448         77.1         104         2         PH1101         Ig light chain           446.5         76.9         112         2         F30538         Ig kappa chain           446.5         76.9         112         2         S26336         Ig kappa chain           445.5         76.7         109         2         S26336         Ig kappa chain           445.5         76.7         114         2         S44119         Ig kappa chain           445         76.6         138         2         A53261         Ig kappa chain           443.5         76.3         132         2         S46373         Ig kappa chain           443.         76.2         103         2         PH1050         Ig light chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         113         2         PL0264         Ig kappa chain           441.5         76.0         114         2         S03304         Ig kappa chain           439.5         75.6         111         2         S03304 <td< td=""><td>31       448       77.1       104       2       PH1101       Ig light chain V r         32       447.5       77.0       112       2       F30538       Ig kappa chain V r         34       445.5       76.7       109       2       S26336       Ig kappa chain V r         35       445.5       76.6       104       2       PH1104       Ig kappa chain V r         37       445       76.6       104       2       PH104       Ig kappa chain V r         39       443       76.2       103       2       PH1050       Ig kappa chain V r         40       44.2       76.1       104       2       PH1050       Ig light chain V r         41       41.5       76.0       113       2       PL0264       Ig kappa chain V r         42       76.1       104       2       PH1050       Ig kappa chain V r         43       430.5       75.6       111       2       S03304       Ig kappa chain V r         43       438.5       75.5       134       I K4H107       Ig kappa chain V r</td></td<>	31       448       77.1       104       2       PH1101       Ig light chain V r         32       447.5       77.0       112       2       F30538       Ig kappa chain V r         34       445.5       76.7       109       2       S26336       Ig kappa chain V r         35       445.5       76.6       104       2       PH1104       Ig kappa chain V r         37       445       76.6       104       2       PH104       Ig kappa chain V r         39       443       76.2       103       2       PH1050       Ig kappa chain V r         40       44.2       76.1       104       2       PH1050       Ig light chain V r         41       41.5       76.0       113       2       PL0264       Ig kappa chain V r         42       76.1       104       2       PH1050       Ig kappa chain V r         43       430.5       75.6       111       2       S03304       Ig kappa chain V r         43       438.5       75.5       134       I K4H107       Ig kappa chain V r

## ALIGNMENTS

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Ig kappa chain V region (A52) - mouse

(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

(Species: Musculus (1960)

(Speci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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90.4%; Score 525; DB 2;
Best Local Similarity 90.1%; Pred. No. 3.9e-39;
Matches 100; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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1 NIMMIQSPSSLAVSAGEKVIMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKILIYWASTR 60

ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEI 111 61 원 ઠે

RESULT 2

19

a

PH1054

fight chain V region (clone 202.135) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000
C;Accession: PH1054
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1054
A;Accession: PH1054
A;Molequle type: mRNA.

A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UP10000176AAE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

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84.0%;
83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: PT0356
A;Molecule type: mRNA
A;Residues: 1-118 <SHE>
                                                                                                                                                                                                                                                                                                              A; Accession: PS0023
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                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S41393 Fr. F; Margaritte, C; Gilbert, D.; Brard, F.; Tron, F. Submittee, C; Gilbert, D.; Brard, F.; Tron, F. Submittee, C; Gilbert, Data Library, January 1994 A;Pescription: Structural characterization of an (NZB X NZW)Fl mouse-derived IgM anti-DN A;Reference number: S41393 A;Accession: S41393 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-112 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Figlibert, D.; Brand, S.; Margaritte, C.; Delpech, A.; Tron, F.

Submitted to the EMBL Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A;Reference number: S42484
A;Accession: S43103
A;Accession: Spealmainary
A;Accession: Spealmainary
A;Molecule type: mRNA
A;Residues: 1-112 <GIL>
A;Across-references: UNIPARC:UPI0000116626; EMBL: Z31353; NID:g467574; PIDN:CAA83231.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                     1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
                                                                                                                             1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
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Species: Mus musculus (house mouse)
Species: Mus musculus (house mouse)
Spacies: 1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
Accession: 843103
                                                                                                                                                                                                                                                                                                                                                 Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
Accession: S41393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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                   Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%; Score 496; DB 2; Length 112; 83.9%; Pred. No. 1.3e-36; ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                           ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYCHQYLSSYTF 103
                                                                                                                                                                                     ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTF 103
Score 498; DB 2; Le
Pred. No. 8.2e-37;
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                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (12.5H VL) - mouse
                 85.7%;
92.2%;
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Matches 94; Conservative
                   Query Match 85.7
Best Local Similarity 92.2
Matches 95; Conservative
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A Molecule type: mRNA

A; Residues: 1-133 < MARA.

B; Experimental source: strain BALB/c

A; Note: the amino-terminal four residues of the mature protein were directly sequenced

C; Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aerugi.

C; Comment: This chain was obtained from a monoclonal in homology

C; Reywords: heterotetramer; immunoglobulin

C; Reywords: heterotetramer; immunoglobulin

B; 1-20/Domain: signal sequence #status predicted <SIG>

F; 21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>

F; 36-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                Ig kappa chain precursor V region (6A4) - mouse (5Species: Mus musculus (house mouse) (5Species: Mus musculus (house mouse) (5Species: Mus musculus (house mouse) (5Accession: PS0023 R) (5Accession: PS0023) (5Accession: PS0023) (5Accession: PS0023) (5Accession: PS0023) (5Accession: PS0023) (6Accession: PS0023) (
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C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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R,Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
C, Exp. Med. 173, 287-296, 1991
A,Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A,Reference number: PT0352; MUID:91108325; PMID:1988536
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ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLEIKR
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A, Note: the authors translated the codon CTT for residue 32 as 6 c, comenent: This protein is an anti-double-stranded DNA antibody C, Superfamily: immunoglobulin V region; immunoglobulin homology F;19-99/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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84.2%; Pred. No. 8.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 488; DB 2;
Pred. No. 7.9e-36;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (2B11.1) - mouse (fragment)
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"grappa chain V-J region (4C8) - mouse (fragment)
"Species: Nus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 12-Peb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 809970
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Riv. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi
A;Reference number: 809955; MUID:90269328; PMID:2347362
A;Accession: 809977
A;Accession: 809977
A;Residues: 1-112 cREI>
A;Residues: 1-112 cREI>
A;Cross-references: UNIPARC;UPI0000115E69; EMBL:X51858; NID:955406; PIDN:CAA36151.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <INM>
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A; Residues: 1-60, T' 62-91, S', 93-101 < CAT>
A; Cross-references: UNIPARC:UP10000115F7F; EMBL:X59193; NID:g52323; PIDN:CAA41903.1; PI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-88 / Domain: immunoglobulin homology < IMM>
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Ig light chain V region - mouse (fragment)

C;Species Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26337; S78449
C;Accession: A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in A;Reference number: S26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-101 <STA>
A;Cross-references: UNIPARC:UPI00001769B0; EMBL:X59193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.3%; Score 478; DB 2;
Best Local Similarity 79.5%; Pred. No. 5e-35;
Matches 89; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Caton, A.J.
submitted to the EMBL Data Library, April 1991
Kreference number: S78447
A;Accession: S78449
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Matches 91; Conservative
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Ig kappa chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C;Accession: 826640; 878098
R;Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, 1895, 1990
A;Title: Nucleotide sequences of the gene/CDNA coding for anti-murine erythrocyte autoan A;Reference number: 809216; MUID:90245589; PMID:2336368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-87, W', 89-138 < OKW>
A; Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT0407

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: PT0407

R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

B, Exp. Med. 173, 731-741, 1991

A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A;Reference number: PT0376; MUID:91147903; PMID:1900082
                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-138 <OKA>
A;Cross-references: UNIPARC:UPI00001769D0; EMBL:X51742
A;Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue
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C;Keywords: heterotetramer; immunoglobulin
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-138/Product: Ig kappa chain (fragment) #status predicted <WAT>
F;41-121/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
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A, Residues: 1-113 < BEH>
A, Cross-references: UNIPARC: UPI0000176A05
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 484; DB 2;
; Pred. No. 1.8e-35;
14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                 R;Okamoto, M. submil Data Library, February 1990 aubmitted to the EMBL Data Library, February 1990 A;Reference number: S78098 A;Accession: S78098
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79.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Simple 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 22/1
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A; Molecule type: mRNA
A; Residues: 1-145 cCHE>
A; Residues: 1-145 cCHE>
A; Residues: 1-145 cCHE>
A; Cross-references: UNIPARC:UPI00001767A7
A; Experimental source: cell line F6-3
C; Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchc C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-134/Product: Ig heavy chain V region (4CII) #status predicted <MAT>
F; 36-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
*Residues: 1-240 <CRD>
A;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:956457; PIDN:CAA34256.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig Kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V-IV region (JI) - human C;Species: Homo sapiens (man) C;Species: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004 C;Accession: A01904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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F;135-145/Domain: constant region (fragment) #status predicted <COR>
                           R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0014
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C;Keywords: signal sequence #status predicted <SIG>
F;21-20/Domain: signal sequence #status predicted <MAT>
F;21-222/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.5%; Score 473.5; DB 2;
79.8%; Pred. No. 1.6e-34;
iive 14; Mismatches 8;
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79.8%;
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Best Local Similarity
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                   C; Dete: 16. Sep-1992 #sequence_revision 16. Sep-1992 #text_change 21-Jan-2000
C; Accession: PL0265
R; Shlomothk, M; Mascelli, M; Shan, H; Radic, M.Z.; Pisetsky, D; Marshak-Rothstein, A
J; Exp. Med. 171, 265-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A; Reference number: PL0231; MUD: 9011618; PMID: 2104919
A; Accession: PL0265
A; Molecule type: mRNA
A; Residues: 1-112 <SHL>
A; Accession: PL0265
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-56 / Domain: immunoglobulin homology <IMM>
F; 24-40/Region: framework 1
F; 16-56 / Region: framework 3
F; 6-56 / Region: framework 3
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R;Hong, H.J; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, B;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, B;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, B;Hille: Cloning and characterization of cDNAs coding for heavy and light chains of a mc A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc A;Reference number: Pc1214

A;Reference number: Pc1213

A;Residues: 1-134 <-KONA

A;Residues: 1-134 <-KONA

A;Residues: 1-134 <-KONA

A;Residues: 1-134 --KONA

A;Residues: 1-134 --KONA

A;Residues: 1-134 --KONA

C;Superfamily: immunoglobulin
C;Reywords: heterotetramer; hemonoglobulin
C;Reywords: hemonoglobulin
C;Reywords
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor V region (F6-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g kappa chain precursor V region (mAb H8) - mouse (fragment)
'Species: Mus musculus (house mouse)
'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
'Accession: PC1214
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80.7%; Pred. No. 1.5e-34;
ive 11; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.9%; Score 476; DB 2;
82.1%; Pred. No. 7.4e-35;
Live 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Region: complementarity-determining 3
C; Species: Mus musculus (house mouse)
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Best Local Similarity 82.1%;
Marches 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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9 80

Gaps

1;

10; Indels

Length 240;

DB 2;

ij 9

Gaps

1;

Indels

Length 145;

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A/Gene: GDB:IGKV
A/Cross-references: GDB:119341; OMIM:146980
A/Map position: 2p12-2p12
A/Introns: 17/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C/Complex: An immunoglobulin V region; immunoglobulin homology
C/Complex: An immunoglobulin V region; immunoglobulin homology
C/Keywords: Heterotetramer; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin predicted <SIG>
F/1-20/Domain: asignal sequence #status predicted <SIG>
F/21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
F/21-43/Region: complementarity-determining 1
F/21-5/Region: complementarity-determining 2
F/21-122/Region: complementarity-determining 3
F/215-122/Region: framework 4
F/23-133/Region: framework 4
F/23-133/Region: framework 4
F/23-114/Disulfide bonds: #status predicted
                                                                                                                                              A;MOJecule type: DNA
A;Residues: 1-133 <KLO>
A;Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00022; GB:X51570; NID:g33
A;Note: the sequence was determined from the differentiated gene
R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G. Wuclaic, Rese. 13, 6815-6529, 1985
Muclaic, Subgroup, IV of human immunoglobulin K light chains is encoded by a single germl A;Reference number: A93589; MUID:86041853; PMID:2997712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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80.7%; Score 469; DB 1; Length 133;
Best Local Similarity 77.0%; Pred. No. 3.6e-34;
Matches 87; Conservative 15; Mismatches 11; Indels
                                                                                                                                       A; Accession: A01904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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Search completed: May 9, 2006, 01:33:51 Job time : 17.1212 secs

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GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                  Copyright
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- protein search, using sw model OM protein May 9, 2006, 01:18:41; Search time 103.461 Seconds (without alignments) 770.577 Million cell updates/sec Run on:

US-10-700-632-8 581 1 NIMLTQSPSSLAVSAGEKVT......CHQYLSSRTFGGGTKLBIKR Title: Perfect score: Sequence:

113

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

1: uniprot\_sprot:\*
2: uniprot\_trembl:\* UniProt 05.80:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

+[::000		* 2			COLUMNIC	
No.		Match	Watch Length DB	DB	ID	Description
¦	469	80.7	133	1	KV4B HUMAN	P06313 homo sapien
~	463.5	79.8	240	7	Q52L64 MOUSE	Q52164 mus musculu
9	458.5	78.9	114	Н	KV4A HUMAN	homod
4	451.5	77.7	134	Н	KV4C_HUMAN	P06314 homo sapien
Ŋ	447.5	77.0	255	~	Q6KB05 MOUSE	Q6kb05 mus musculu
9	421	72.5	121	Н	KV40 HUMAN	homod
7	400.5	68.9	109	7	KV4D HUMAN	homod
<b>&amp;</b>	384	66.1	109	7	Q9UL78 HUMAN	Q9ul78 homo sapien
σ	382	65.7	129	-	KV3L HUMAN	P18135 homo sapien
0	376.5	64.8	114	-	KV1A MOUSE	P01632 mus musculu
11	376	64.7	107	~	Q96SA9 HUMAN	Q96sa9 homo sapien
۲,	374	64.4	109	-	KV3E HUMAN	homo
m	373.5	64.3	108	ď	Q9UL70 HUMAN	Q9ul70 homo sapien
14	372	64.0	109	-	KV3B HUMAN	P01620 homo sapien
r.	371	63.9	129	-	KV3M HUMAN	homo
9	370	63.7	109	Н	KV3D_HUMAN	рошо
7	370	63.7	235	7	Q6GMV9 HUMAN	homo
8	367.5	63.3	136	Н	KVSB MOUSE	mus m
σ,	367.5	63.3	236	7	Q6P5S8 HUMAN	Q6p5s8 homo sapien
0	367.5	63.3	238	7	Q58EU4_MOUSE	mus m
_	367	63.2	109	~	Q9UL85 HUMAN	рошо
~	366.5	63.1	236	~	Q6PIL8_HUMAN	homod
23	365.5	62.9	66	7	Q9JL74_MOUSE	mus r
4	364.5	62.7	149	-	KV5A MOUSE	P01633 mus musculu
ω.	363.5	62.6	108	-	KV1M_HUMAN	P01605 homo sapien
9	362.5	62.4	108	~	Q9UL79_HUMAN	рошо
7	361	62.1	109	Н	KV3G HUMAN	рошо
œ	360.5	62.0	236	~	Q6PIH7 HUMAN	рошо
6	360	62.0	101	~	Q9UL81_HUMAN	рошо
0	360	62.0	129	Н	KV3H HUMAN	P04207 homo sapien
_	359.5	61.9	108	7	KV1V HUMAN	P04430 homo sapien

Q9ul77 homo sapien									Q9ul86 homo sapien				
Q9UL77 HUMAN	NV3F HUMAN	KV3P_MOUSE	Q6GMW0_HUMAN	Q6PJF2 HUMAN	KV3L MOUSE	KV3R_MOUSE	Q6PIH6 HUMAN	Q5F2I7 MOUSE	Q9UL86_HUMAN	KV1Y HUMAN	Q6PITS HUMAN	Q66JS7_MOUSE	Q8NEK0_HUMAN
۸ -	٠.	4	~	~	н	н	~	N	~	н	N	~	8
108	100	110	235	235	111	111	240	111	109	108	236	238	239
61.9	01.0	61.8	61.8	61.8	61.7	61.7	61.7	61.2	61.1	61.0	61.0	61.0	8.09
359.5	000	359	359	359	358.5	358.5	358.5	355.5	355	354.5	354.5	354.5	353
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## ALIGNMENTS

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g kappa chain V-IV region JI precursor.
Homo sapiens (Human)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE-86041853; PubMed-2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Subgroup IV of human immunoglobulin K light chains is encoded single germline gene."; Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-IV region JI. Framework-1. Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-3. Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 200022; CAA77317.1; -; Genomic_DNA.
PIR; A01904; K4HUJI.
HSSP; POL625; L1VR.
SMR; P06313; 2.11.73.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:000582; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14633 MW; SFB3953066744AF4 CRC64;
                                      133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
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                                      PRT;
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
133
43
60
60
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114
1122
1132
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133
133 AA;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                      KV4B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zachau H.G.
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NON TER
SEQUENCE
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KV4B HUMAN

ID KV4B HUMAN

ID 10-JAN

DT 10-JAN

DE 19 kapp

SS HOMO SI

OC BUKARIY

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RA KIODECIN

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OC C TEMO WE

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80.7%; Score 469; DB 1; Length 133;

Query Match

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21
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REGION
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                                                                                                                                                                                                                                                                                                                                                         RESULT 3
KV4A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGION
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XX TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altschul S.F., Zeeberg B.B., Bactow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B.B., Bactow K.H., Schaefer C.F., Bhat N.K.,

XA Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XA Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

XA Baba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XA Bosak S.A., McEwan P.J., NcKernan K.J., Lu X., Gibbs R.A.,

XA Nilalon D.K., Marush D.M., Sodergran B.J., Lu X., Gibbs R.A.,

XA Nilalon D.K., Marush D.M., Madan A., Rodrigues S., Sanchez A.,

XA Haby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XA Nilalon D.K., Marow J.M., Grens B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schwuz J., Myers R.M.,

Schnerch A. Schein J.B., Jones S.J.M., Marra M.A.,

Schnerch A. Schein J.B., Jones S.J.M., Marra M.A.;

Tand mouse CDNA sequences.",
                               ö
                                                                                          9
                                                                                                                                              80
                                                                                                                         21 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                          1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                  Gaps
                                                                                                                                                                                                             61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTPGGGTKLEIKR 113
                                                                                                                                                                                                                                            81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYDTIPTFGGGTKVEIKR 133
                                  .,
                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26609 MW; CF8630CCC002E52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
77.0%; Pred. No. 5.7e-42;
ive 15; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -; mRNA
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, 613-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 14) Phypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC094049; AAH94049.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q52L64_MOUSE PRELIMINARY;
                           87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
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   Best Local Similarity
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Length 240;

DB 2;

79.8%; Score 463.5;

Query Match

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                   1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                   61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLEIKR 113
                                                                                                                                                                                               Schneider M., Hilschmann N.;
"The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
SMART; SMOG406; IGv. 1.
PROSITE; PS50335; IG LIKE; 1.
3D-structure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-3. Framework-4.
By similarity.
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                           Indels
  77.2%; Pred. No. 4.4e-41; tive 15; Mismatches 10;
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PDB; 1EEQ; X-ray; A/B=1-114.
PDB; 1EKG; X-ray; A/B=1-114.
PDB; 1EKG; X-ray; A/B=1-114.
PDB; 1EVE; X-ray; Ø=1-114.
PDB; 2LVE; X-ray; Ø=1-114.
PDB; 3LVE; X-ray; Ø=1-114.
PDB; 3LVE; X-ray; Ø=1-114.
PDB; 5LVE; X-ray; A/B=1-114.
PDB; 5LVE; X-ray; A/B=1-
                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kappa chain V-IV region Len.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                       114 AA
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                             88; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
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P01625;
21-JUL-1986 (
01-OCT-1996 (
10-MAY-2005 (
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STRAIN-Balb/c;
A Briand Jr. P., Hoebeke J.;
A Modulation of the Maucarinic acetylcholine receptor activity with monoclonal anti-M2 receptor antibody fragments.";
J. Biol. Chem. 279:55697-55706 (2004).
B Biol. Chem. 279:55697-55706 (2004).
B REMBI, AJ7461809, CAG34081.1; -; Other_DNA.
DR RISP: PO1837; IKCR.
DR InterPro; IPR001359; IG.
DR InterPro; IPR001359; IG.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                 61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLEIKR 113
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O
                                                                                                                                                                                                                                                         77.7%; Score 451.5; DB 1; Length 134; 74.6%; Pred. No. 4.2e-40; ive 15; Mismatches 13; Indels 1.
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                                                                           chain V-IV region B17
                                                                                                         Complementarity-determining-1.
                                                                                                                                      Complementarity-determining-2.
                                                                                                                                                     Framework-3.
Complementarity-determining-3.
SMART; SM00406; IGv; 1.—
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                              14966 MW; 6413A22FD0738832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
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Last annotation update)
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By similarity.
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Name=scFv B8E5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                       Local Simitatry
hes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEKBOS; MOUSE PRELIMINARY; QEKBOS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                                                                                                                                                                                                                              134 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVWIQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPQQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                               1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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                                                                                                                                                                                                                                                                                                                                    ; Score 458.5; DB 1; Length 114;
; Pred. No. 6.3e-41;
15; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      12640 MW; 0647F1D17F236485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-ARR-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-IV region B17 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMR; P06314; 21-134.

GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 13:6531-6544 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X02990; CAA26733.1; -; mRNA.
HSSP; P01625; 1LVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
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76.3%;
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    [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                        114 AA;
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   KV4C HUMAN
P06314;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
197 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSY--PLTFGAGTKLEIK 249
                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE-86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D..
                                                                                                                                                                                                                         Subgroup IV of human immunoglobulin K light chains is encoded by
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Complementarity-determining-1.
Framework-2.
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Complementarity-determining-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-IV region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13380 MW; 9586AD4188D33974 CRC64;
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                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-IV region precursor (Fragment).
Name-IGKV4-1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                   HGNC; HGNC: 5834; IGKV4-1.

GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                 121 AA
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PIR; A01902; K4HU.
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SMR; P06312; 21-121.
Ensembl; ENSG0000153586; Homo sapiens.
                                                 PRT;
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Matches 77; Conservative
                                                STANDARD;
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RESULT 7

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Homo sapinas (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                          Olsen K.E., Sletten K., Westermark P.,
"Extended analysis of AL-amyloid protein from abdominal wall
subcutaneous far biopsy: kappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245:713-716(1998).
-i- FUNCTION: May play an important role in fibrillogenesis.
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                                                                                                                                                                                                                                                                                                    TISSUE=Abdominal adipose tissue;
MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1.
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSTIE; P850835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                           annotation update)
109 AA
                                                                   (Rel. 42, Last sequence update) (Rel. 47, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
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                                                                                                                 Ig kappa chain V-IV region STH (Fragment)
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                                             (Rel. 42, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL78 HUMAN PRELIMINARY;
Q9UL78;
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les 75; Conserv
                                                                                                                                                                                                                                                                              PROTEIN SEOUENCE.
                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                           10-OCT-2003
                                                                 10-OCT-2003
10-MAY-2005
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IMLTOSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE
                                                                                                                                                                                                                                                                                                            MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840; Kippp T.J., Tomhave E., Chen P.P., Careon D.A.; "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic
                SGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSS-RTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation. Implications for etiology and immunotherapy.";
J. Bxp. Med. 167:840-852(1988).
-1- DISBASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 382; DB 1; Length 129;
; Pred. No. 1.1e-32;
18; Mismatches 13; Indels
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Complementarity-determining-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                      01-NOV-1990 (Rel. 16, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) II Kappa chain V-III region HAH precursor. Homo sapiens (Human).
                                                                                                          129 AA.
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                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
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                                                                                                          STANDARD;
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HSSP; P01625; 1EEQ.
SMR; P18135; 21-129.
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129 AA;
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                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                        leukemia.
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                            Wagner S.D., Luzzatto L.;
"V Kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
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                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                        MEDLINE=98277]39; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                Pubmed-15.

Pubmed-15.

Martin T., Duffy S.F., Carson D.A., Kipps T.J.;

"Buidence for somatic selection of natural autoantibodies.";

"Exp. Med. 175:983-991(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
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                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
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68.1%; Pred. No. 5.4e-33;
ive 18; Mismatches 12;
                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 23:391-397(1993).
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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D30607.
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H30607.
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PubMed=1373487;
                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                               SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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S34096; S34096.
; P01625; 1EK3.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claflin J.L., Berry J.;
"Genetics of the phosphocholine-specific antibody response to
Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81241357; PubMed=6788890; DOI=10.1084/jem.153.5.1366; Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.; "Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLRIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YIGVPDRFTGSGSGTDFTLTISSVQVEDLTHYYCAQFYSYPLTFGAGTKLELKR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-2. Framework-3. Complementarity-determining-3. Framework-4.
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16; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mus musculus (Mouse).
                                                                                 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 141:4012-4019(1988).
-!- FUNCTION: Anti-phosphocholine antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSMUSG0000052500; Mus musculus.
                                                                                 PRT;
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PIR; A01915; KVMS7A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Exp. Med. 153:1366-1370(1981)
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InterPro, IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 1-113
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hes 76; Conservative
                                                                                 STANDARD;
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SMR; P01632; 1-114
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                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chains."
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                                                                                       SOLITIFIE IN THE PRINCE OF COURT SET OF SET 
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
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                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98375893; PubMed=9712075; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."; Jimmunol. 161:2020-2031(1998).
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107 AA
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InterPro; IPR003596; Ig v.
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                 variable region (Fragment).
Homo sapiens (Human).
HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
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PIR, 534083, 534083.
PIR, 534086, 534086.
HSSP, PO1607, 1BWW.
SMR, Q96SA9; 1-107.
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Pubmed=1903706;
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KV3E HUMAN

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group.";
Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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                                                                                                                                                                                                                                                               'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSS-RTFGGGTKLEIKR
                                                                                                                                                                                                        MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characteristics of antibodies bearing an anti-DNA-
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%; Score 373.5; DB 2;
64.9%; Pred. No. 7e-32;
tive 17; Mismatches 16;
                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998)
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-III region SIE.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                              associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
EMBL, ARO35044, AAD56280.1; -; mRNA.
PIR, PHO863: PHO863.
HSSP, PO1607; 1BWW.
SWR; Q9UJ/0; 1-108.
InterPro; IPR001519; Ig-like.
InterPro; IPR001596; Ig-v.
SWART; SM00406; IGV: 1.
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                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 74; Conservat
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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P01620;
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NON TER
SEQUENCE
                                                          (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.
                                                                                                                                                                                                                                                                                                                                 nomo papera. Mutazoa.
Bukaryota, Metazoa. Ghordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                     PROTEIN SEQUENCE.
MEDLINE-22046598; PubMed-6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 11746 MW; 566C115E6B9CBEEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGv; 1.—
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
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SMR; P01623, 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                          109 AA
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Q9UL70 HUMAN PRELIMINARY;
Q9UL70;
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Matches 72; Conservative
                                                                                                                                                                                                        STANDARD;
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RESULT 13 Q9UL70 HUM ID Q9UL7 AC Q9UL7 DT 01-MA

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Length 108;

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Job time : 103.461 secs
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                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Burchontoglires; Primates; Catarrhini; Hominidae;
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MEDILINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
Kippp T.J., Tomhave E., Chen P.P., Carson D.A.;
Matcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167-840-852(1988).
-i- DisBass: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSS-RTFGGGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                     OGG: GO: 00005576; C: extracellular region; NAS. GO: GO: 0003823; F: antigen binding; NAS. GO: GO: 0000855; F: antigen binding; NAS. InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SNART; SN00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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HSSP; P01625; 1EEQ.
SMR; P18136; 21-129.
ENGEMBL; ENSG0000169769; Homo sapiens.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.0%; Score 3/2; 55.28
Best Local Similarity 62.8%; Pred. No. 1e-31, Matches 71; Conservative 22; Mismatches
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SMR; P01620; 1-109
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NCBI_TaxID=9606;
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DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR SMART; SM00406; Ig_v.

DR SMART; SM00406; IG_v; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; Signal.

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; Pred. No. 1.6e-31;
18; Mismatches 14;
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Sequence 2, Appli
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1 NIMLTQSPSSLAVSAGEKVT......CHQYLSSRTFGGGTKLBIKR
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-010-146-096A-15

US-07-916-096A-15

US-08-435-400-34

US-08-353-400-34

US-08-353-400-37

US-08-353-400-37

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Gapop 10.0 , Gapext 0.5
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Sequence 189, Applications of		ON HUMAN MONONUCLEAR PHAGOCYTES ON HUMAN MONONUCLEAR PHAGOCYTES PCT/US93/10384 993	Length 112; Indels 0; Gaps 0;	YQQIPGQSPKLLIYWASTR 60                     YQQKPGQSPKLLIYWASTR 60	TPGGGTKLEIK 112               TPGGGTKLEIK 112
114 2 US-08-929-856-189 113 4 PCT-US93-08435-6 113 4 PCT-US93-08435-6 113 4 PCT-US93-08435-6 110 2 US-08-957-001B-5 110 2 US-08-957-001B-24 110 2 US-08-957-001B-24 110 2 US-09-496-301-24 111 2 US-07-916-098A-56 114 2 US-07-916-098A-56 115 2 US-07-916-098A-56 116 2 US-09-495-880A-11 113 2 US-09-495-880A-11 113 2 US-09-195-516-4 113 2 US-09-188-082-14 105 09-188-082-14 105 09-188-082-14 105 09-108-09-14	ı	ANTIBOD BULIN G -DOS 3377.4; 02-NOV-1	8%; Score 539; DB 2; 0%; Pred. No. 1.7e-46; 6; Mismatches 3;	NIMITOSPSSIAVSAGEKVTMSCKSSOSVFFSSSOKNYIAWYQOIPGOSPKILIYWASTR   ::	ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLRIK
288 289.6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		RESULT 1  US-084-435-516-28  US-084-435-516-28  Sequence 28, Application US/08435  Patent No. 650031  GENERAL INFORMATION: PAPLICANT: TITLE OF INVENTION: IMMUNOBLO NUMBER OF SEQUENCES: 28  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS; SOFTWARE: ASCII Lext CURRENT APPLICATION DATA: APPLICATION NUMBER: UK 92 2 FILING DATE: 04-NOV-1992; - CLASSIPICATION: 424 PRIOR APPLICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: ATTOLA BECKET NUMBER: MX TELECOMMUNICATION INFORMATION: TELEDERAL: (617) 227-7400 TELEBRAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 112 amino acids TYPE: amino acid TYPE: amino acid FRAGMENT TYPE: internal US-08-435-516-28	Query Match Best Local Similarity 92. Matches 103; Conservative		Qy 61 ESGVPDRFTGSC              bb 61 ESGVPDRFTGSC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: GU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/0879
CURRENT FILING DATE: 1998-11-17
CURRENT FILING DATE: 1998-11-17
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: WG 60/013,709
EARLIER APPLICATION NUMBER: US 60/013,709
EARLIER APPLICATION NUMBER: US 60/013,709
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NIMLTOSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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89.4%; Pred. No. 1.4e-44;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 520; DB 2; Length 113;
Pred. No. 1.4e-44;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
                                                                                                                                                            FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BETHARD D.
RECISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18/33/463/IMIN
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.46
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09155107
Patent No. 6254868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 113 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.43
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 89.4
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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ORGANISM: Murine
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Weahington, D.C.
COUNTRY: USA
                                                                                         GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Ham
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES:
ADDRESSEE: FOLLY & Lardner
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Pred. No. 1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION NUMBER: US/08/690,102A
FILING APPLICATION: 424
PRIOR APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTONNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                 STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA_
ZIP: 20007-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             Sequence 2, Application US/08690102A
Patent No. 5789554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.5%;
89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 89.49
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
    RESULT 2
US-08-690-102A-2
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US-09-127-902-2
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BINELY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.

APPLICANT: THOMAS, DAVID W.

APPLICANT: ROSA, WARGARET D.

APPLICANT: ROSA, JOSEPH J.

TITLE OF INVENTION: ANTI-CAS ANTIBODY HOMOLOGS USEFUL IN

TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
                                1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSGNQKNYLAWYQQKPGQSPELLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPSSLAVSVGEKVTMICKSSQSLLYSTNQKNYLAWYQQKPGQSPKLLIYWASTR 60
     1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                             61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
                                                                                                                                         ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYRTFGGGTKLEIKR 113
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84.8%; Pred. No. 6.8e-43;
tive 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIT. 0000
CALT. 0000
CALT. 0000
CARDUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION TORDATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSES: ALLEGRETTI & WITCOFF, LTD.
ADDRESSES: 10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                     US-07-916-098A-15; Sequence 15, Application US/07916098A; Patent No. 5871732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 112 amino acids
amino acid
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Best Local Similarity 84.8%
Best Local Similarity
Percentage
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: CHICAGO
STATE: ILLINOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-916-098A-15
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                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DCT/US95/09641
FILING DATE: 11-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YUHAN CORPORATION

APPLICANT: YUHAN CORPORATION

TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV

TITLE OF INVENTION: A S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REPERBUCE: OV17440

CURRENT APPLICATION NUMBER: US/10/146,305

CURRENT FILING DATE: 2002-05-15

PRIOR APPLICATION NUMBER: KR 10-2001-26634

PRIOR FILING DATE: 2001-05-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: KOPATENTIN 1.71
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1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                             61 ESGVPDRFTGSGSGTDFTLTISRVQVBDLAIYYCHQYLSSWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPDRFTGSGSGTDFTLTISRVQVEDLAIYYCHQYLSSWTFGGGTKCLEIKR 113
                                                                               61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
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89.4%; Pred. No. 1.4e-44;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.9%; Score 505; DB 2; Length 130; Best Local Similarity 84.1%; Pred. No. 5.1e-43; Matches 95; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                    PCT-US95-09641-2; Sequence 2, Application PC/TUS9509641; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10146305
Patent No. 6939956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Escherichia coli
US-10-146-305-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.4
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-09641-2
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TYPE: PRT
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                                      APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCES
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19477
ZIP: 19477
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 498.5; DB 4;
Pred. No. 1.9e-42;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PREPLICATION DATA:
PREPLICATION DATA:
PILING DATE: 09-SEP-192
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 36C P50107
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRARACTERISTICS:
TENDENCE CHRARACTERISTICS:
Sequence 4, Application PC/TUS9308435 GENERAL INFORMATION:
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85.8%;
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amino acid
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Best Local Similarity 85.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       Spring House
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                     CITY: Spr
STATE: PA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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Sequence 115, Application US/09419788 Patent No. 6825325

US-09-419-788-115

GENERAL INFORMATION:

APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
APPLICANT: NAHRING, Jorg
APPLICANT: SACK, Markus
APPLICANT: MONECKE, Michael
APPLICANT: LIAO, Yu-Cai
APPLICANT: SPIEGEL, Holger
APPLICANT: ZIMMERMAN, Sabine

1 NIMLIQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR Gaps APPLICANT: EMANS, Neil

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Resistance
FILE REPERENCE: 0147 0189P
CURRENT APPLICATION WHBER: US/09/419,788
CURRENT APPLICATION WHBER: 98 11 9630.6 EP
EARLIER APPLICATION WHMBER: 98 11 9630.6 EP
EARLIER PILING DATE: 1998-10-16
EARLIER PILING DATE: 1998-10-16
SARIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 115
LENGTH: 259 ) OTHER INFORMATION: Description of Artificial Sequence: synthetic, no ) OTHER INFORMATION: natural origin US-09-419-788-115 ö US-08-929-856-66

US-08-929-856-66

Sequence 66, Application US/08929856

Patent No. 6136568

GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Rose, Floyd
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
TITLE OF INVENTION: ROLLING TEMPLATES

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS: Query Match 85.7%; Score 498; DB 2; Length 259; Best Local Similarity 84.1%; Pred. No. 5.6e-42; Matches 95; Conservative 10; Mismatches 8; Indels OFFRAING SYSTEM: PC-DOS/MS-DOS OFFWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,856 FILING DATE: 15-SEP-1997 CLASSIFICATION: 536 ATTONREY/AGBNT INPORMATION:
NAME: FOLEY, Shawn P. REGISTRATION NUMBER: 33,071 REFERENCE/POCKET NUMBER: 33,071 TELECOMMULCATION INFORMATION: TELECOMMULCATION: TELEPHONE: 908-654-5000 ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ ADDRESSEE: MENTILLIK MENTILIK
JIKET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS ORGANISM: Artificial Sequence LENGTH: 114 amino acids TELEFAX: 908-654-7866 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: FYPE: amino acid
FOPOLOGY: linear

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21 DIVMSQSPSSLAVSAGEKVIMSCKSSQSLLNSRTRKNYLAWYQQRPGQSPK1LIYWASTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RSGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 488; DB 1; Length 239;
Pred. No. 5.1e-41;
9; Mismatches 9; Indels
      PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pillsbury Winthrop, L.L.P. STREET: 1100 New York Ave., N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acid8
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Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <unbelled to the control of t
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-423-439-38
                                                                                                                         CLASSIFICATION: 424
CLASSIFICATION DATA:
RAPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-UNA-1994
INFORMATION FOR SEG ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.18;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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      SOFTWARE:
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                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIKR 113
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                                                                                             Ouery Match 84.0%; Score 488; DB 2; Length 114; Best Local Similarity 83.2%; Pred. No. 2.2e-41; Matches 94; Conservative 11; Mismatches 8; Indel8
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Pred. No. 4.6e-41;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/353,400 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08353400; Patent No. 5665357; GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08353400 Patent No. 5665357 GENERAL INFORMATION:
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Best Local Similarity 84.1%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
      , MOLLECUS-08-08-66
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US-08-353-400-37
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                                                                                     1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NIMLIQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 TSGVPDRPTGSGSGTDFTLTISSVQAEDLAIYYCKQSYTLRTFGGGTKLEIKR 269
                                                                                                                                                                    61 BSGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLBIKR 113
                                                                                                                                                                                         219 TSGVPDRFTGSGSGTDFTLITSSVQAEDLAIYYCKQSYTLRTFGGGTKLEIKR 271
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        DB 2; Length 288;
      83.8%; Score 487; DB 2; Length 28
85.0%; Pred. No. 8e-41;
ive 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                          | Sequence 32, Application US/09423439
| Patent No. 6339070
| GENERAL INFORMATION:
| APPLICANT: EMERY, Stephen Charles
| TITLE OF INVENTION: CHEMICAL COMPOUNDS
| NUMBER OF SEQUENCES: 60
| CORRESPONDENCE ADDRESS:
| STREET: 1100 New York Ave., N.W. CITY: Washington
| STATE: D.C. CONTRY: U.S.A.
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APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WOR'D
CURRENT APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <UNKNOWN>
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STRANDEDMESS: single
FOPOLOGY: linear
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Query Match
Best Local Similarity 85.0°
Matches 96; Conservative
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Sequence 76, Application US/08428257A Patent No. 5885808 GENERAL INFORMATION: APPLICANT: Eponet, Robert A. APPLICANT: Epenetos, A.A.

US-08-428-257A-76

RESULT 15

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1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKIYLAWYQQKPGQSPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                   1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
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; Pred. No. 3.8e-41;
10; Mismatches 9; Indels 1:
                                                                             Compounds to target cells
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Job time : 26.4372 secs
         NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
DADRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
                                                                                                                                                                                                                                                                                                         83.6%;
82.5%;
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.5%
                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-428-257A-76
FITLE OF INVENTION:
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Appliant App
                                                                                                                                                      May 9, 2006, 01:57:07; Search time 84.8723 Seconds (without alignments) 556.303 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
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US-10-700-632-62

US-11-004-639-4

US-11-004-639-10

US-11-004-639-14

US-11-004-639-14

US-11-004-639-14

US-11-004-639-14

US-11-004-639-14

US-11-004-639-14

US-11-004-639-14

US-11-008-633-14

US-10-056-052-16

US-10-056-052-16

US-10-056-052-14

US-10-056-052-14

US-10-056-052-14

US-11-089-511-14

US-11-089-511-14

US-11-088-570-14

US-11-088-570-14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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No.
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ADMINITY IMMUNOSEN, INC.

TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REPERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT FILING DATE: 2003-11-05
PRIOR PILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin version 3.2
SEQ ID NO 62

9

ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113

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US-10-700-632-62
, Sequence 62, Application US/10700632
, Publication No. US20050118183A1
, GENERAL INFORMATION:

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DEBLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REPRENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT APPLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
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100.0%; Pred. No. 1.7e-44;
iive 0; Mismatches 0;
US-11-013-537-1

US-09-894-833-2

US-09-898-0135-2

US-09-898-0135-2

US-10-46-689-2

US-10-78-278-2

US-10-974-678-2

US-10-974-678-2

US-10-66-052-18

US-10-467-253-14

US-10-467-253-14

US-10-80-89-56

US-10-80-89-63

US-10-861-662-56

US-10-861-662-63

US-10-861-662-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10700632; Publication No. US20050118183A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ORGANISM: Mus musculus
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     113;
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; ORGANISM: Mus Musculus
US-11-004-659-4
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                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                             61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                  61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
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Sequence 4, Application No. US2005031292641

GENERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TILE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
TILLE OF INVENTION: ASSOCIATED ANTIGEN SM5-1 AND USES THEREOF
FILE REFERENCE: 54906200100
CURRENT APPLICATION NUMBER: US/11/004,659
CURRENT APPLICATION NUMBER: US/12,949
PRIOR APPLICATION NUMBER: US/10/722,949
PRIOR PLIING DATE: 2003-11-26
PRIOR PLIING DATE: 2003-11-26
PRIOR FILING DATE: 2003-3-10-6-6
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 4
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10722849

Publication No. US2050031617A1

Sequence 4, Application US/10722849

Publication No. US2050031617A1

APPLICANT: MA. USION

TITLE OF INVENTION: ANYIBODIES SPECIFIC FOR CANCER

TITLE OF INVENTION: ASSOCIATED ANYIGEN SMS-1 AND USES THEREOF

PILE REFERENCE: 54905200100

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US/10/722,849

CURRENT FILING DATE: 2003-10-26

PRIOR FILING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                               Length 114;
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                                                                                                                                       0; Indels
                                                                                                 Score 581; DB 5;
Pred. No. 1.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 545; DB 5;
Pred. No. 2.9e-41;
                                                                                               Query Match
100.0%; Score 581; D
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 113; Conservative 0; Mismatches
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Best Local Similarity 92.0°
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-722-849-4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62
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                                                                                                                                          1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
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; Sequence 10, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: $4906200200
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; FRIOR PILING DATE: 2003-11-26
; PRIOR PILING DATE: 2003-11-25
; PRIOR FILING DATE: 2003-11-25
; RICH APPLICATION NUMBER: CN 2003101199300
; RICH FILING DATE: C003-06-13
; NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10723003
; Sequence 10, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT APPLICATION NUMBER: CA 2003101199300
; RIOR PILING DATE: 2003-11-25
; PRIOR PILING DATE: 2003-06-13
; RIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE PESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.8%; Score 545; DB 5; Length 133; Best Local Similarity 92.0%; Pred. No. 3.4e-41; Matches 104; Conservative 5; Mismatches 4; Indels
     Length 113;
                                                      4; Indels
Score 545; DB 6;
Pred. No. 2.9e-41;
5; Mismatches 4;
  93.8%;
92.0%;
                                                         Matches 104; Conservative
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ORGANISM: Mus musculus
                            Similarity
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  Query Match
Best Local S
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PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR FILING DATE: 2003-11-25
PRIOR PILING DATE: 2003-6-13
PRIOR PILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PASLESEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 239
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-11-004-639-34
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APPLICANT: WA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: PARTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-6-13
PRIOR FILING DATE: 2003-6-13
PRIOR FILING DATE: 2003-6-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGH: 239
                                                                                                                                                                                                                                                                                                                                                       61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR
                                                                                                                                                                  Query Match 93.8%; Score 545; DB 6; Length 133; Best Local Similarity 92.0%; Pred. No. 3.4e-41; Matches 104; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.8%; Score 545; DB 5; Length 239; Best Local Similarity 92.0%; Pred. No. 6.2e-41; Matches 104; Conservative 5; Mismatches 4; Indels
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APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT PILING DATE: 2004-12-02
PRIOR FILING DATE: 2003-11-26
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/11004639; Publication No. US20050232931A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/10723003
Publication No. US20040254108A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                            ; ORGANISM: Mus musculus US-11-004-639-10
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US-11-004-639-14
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                                                                                                                                                                                                                                   1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | APPLICANT: MA, Jing |
| TITLE OF INVENTION: PREPARATION BIFUNCTIONAL FUSION PROTEINS |
| TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS |
| FILE REFERENCE: 549662000200 |
| CURRENT APPLICATION NUMBER: US/10/723,003 |
| CURRENT PILING DATE: 2003-11-26 |
| PRIOR PILING DATE: 2003-11-25 |
| PRIOR FILING DATE: 2003-11-25 |
| PRIOR FILING DATE: 2003-6-13 |
| NUMBER OF SEQ ID NOS: 68 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NOS: 4 |
| LENGTH... 661
                                                                                                Query Match 93.8%; Score 545; DB 6; Length 239; Best Local Similarity 92.0%; Pred. No. 6.2e-41; Matches 104; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.8%; Score 545; DB 5; Length 661; Best Local Similarity 92.0%; Pred. No. 1.7e-40; Matches 104; Conservative 5; Mismatches 4; Indels
OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic Construct
US-10-723-003-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 34, Application US/10723003; Publication No. US20040254108A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/11004639; Publication No. US20050232931A1; GENERAL INFORMATION:
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, APPLICANT: GUO, Yajun
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SEQ ID NO 31
LENGTH: 112
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Sequence 10, Application US/10056052

GENERAL INFORMATION:

APPLICANT: PATII, Joseph M

APPLICANT: HUTCHINS, Jeff T

APPLICANT: PATII, Paul

APPLICANT: PAUL

APPLICANT: PAUL

APPLICANT: PAUL

FILING DATE: 2001-04-19

FRIOR PILING DATE: 2001-06-18

PRIOR PILING DATE: 2001-03-12

SOFTWARE: PETENTON VUMBER: 60/264,072

PRIOR PILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 20

SECTIONAL IN PATILICATION VERSION 3.1

SECTIONAL IN PATILICATION PATIS

SECTIONAL IN PATILICATION PATIS

SECTIONAL IN PATILICATION PATIS

SECTIONAL IN PATILICATION PATIS

PRIOR PILING DATE: 2001-03-12

SECTIONAL IN PATILICATION PATIS

SOFTWARE: PATING PATILICATION PATIS

PRIOR PILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113
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TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: $49062000200
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/10/723,003
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR APPLICATION NUMBER: CN 201292999
PRIOR PILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.6%; Score 544; DB 4; Length 112; Best Local Similarity 92.9%; Pred. No. 3.6e-41; Matches 104; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 661;
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93.8%; Score 545; DB 6;
Best Local Similarity 92.0%; Pred. No. 1.7e-40;
Matches 104; Conservative 5; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-056-052-10
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                                                                                   US-10-816-938-31
US-10-816-938-31
Sequence 31, Application US/10816938
FUBLICATION NO. US20040229301A1
GENERAL INFORMATION:
TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                       Score 544; DB 5; Length 112;
Pred. No. 3.6e-41;
5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.9%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PATTI, JOSEPH M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
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Best Local Similarity 92.04
Matches 103; Conservative
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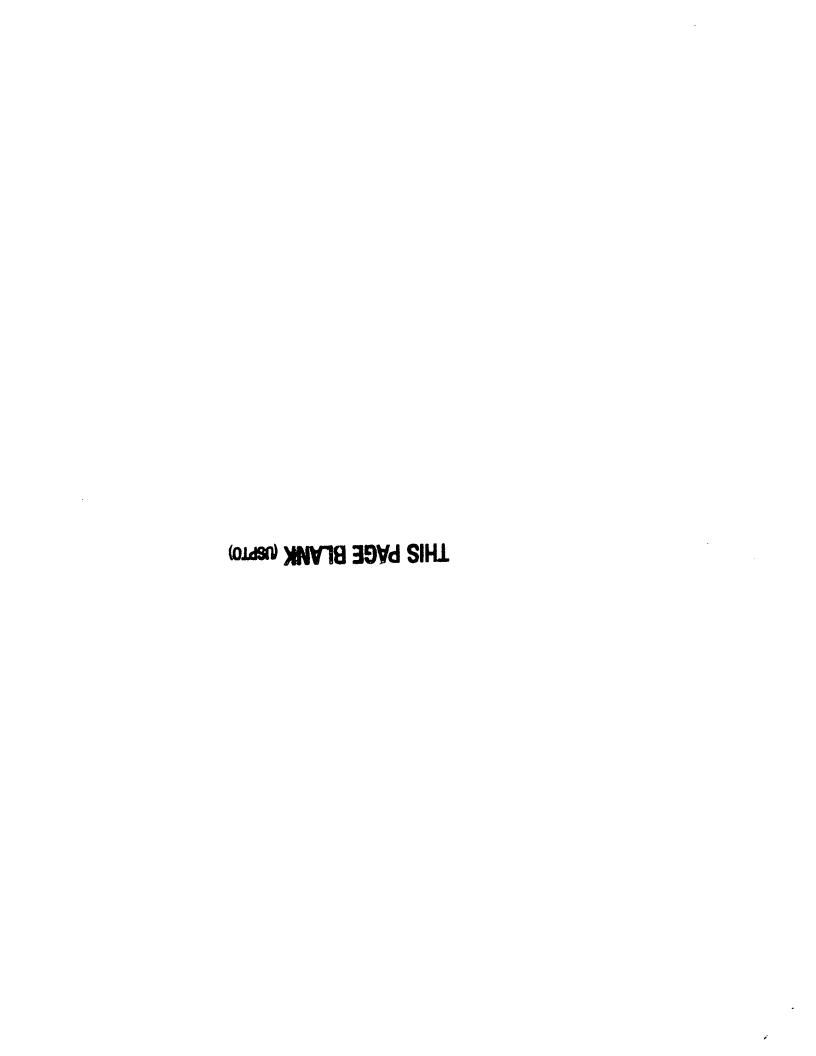
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1 NIVMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
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Pred. No. 1e-40;
6; Mismatches 3; Indels
                                                                                     TOPOLOGY: linear

MOLECULE TYPE: peptide

FRACHENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28
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                     INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
  TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                   Query Match 92.8%;
Best Local Similarity 92.0%;
Matches 103; Conservative
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Job time: 84.8723 secs
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TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REFERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT APPLICATION NUMBER: 2004-11-05
PRIOR PLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2002-11-07
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Publication No. US20030144483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IVLTQSPGSLAVSPGRRVIMSCKSSQSVFFSSSQRNYLAWYQQIPGQSPRLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region US-10-700-632-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.5%; Score 543; DB 5; Length 113; 93.8%; Pred. No. 4.4e-41; tive 3; Mismatches 4; Indels
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CITY: Annandale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-ANG-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
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NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                      Sequence 10, Application US/10700632
Publication No. US20050118183A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 28
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COUNTRY: USA
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Best Local Similarity 93.88
Matches 105; Conservative
                                                                                                                                -10-700-632-10
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Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 71, Appl Sequence 11, Appl Sequence 17, Appl Sequence 13, Appl Sequence 11, Appl Sequence 13, Appl Sequence 27, Appl Sequence 13, Appl Sequence 23, Appl Sequence 26, Appl

Scoring table:

Searched:

Database

Title: Perfect score:

Sequence:

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Run on:

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1 NIMLTOSPSSLAVSAGEKVTMSCKSSOSVFFSSSOKNYLAWYQOIPGOSPKLLIYWASTR 60
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APPLICANT: HUTCHINS, Jeff T
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANNI, Paul
APPLICANT: PATL, Practisha
APPLICANT: PATL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P07065040540, SAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT PILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/056,052
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
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PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PELING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFFWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.6%; Score 544; DB 11; Length 112; Best Local Similarity 92.9%; Pred. No. 2.5e-33; Matches 104; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                            | US-11-202-507A-11
| US-11-202-507A-5
| US-10-771-257-27
| US-10-834-397-17
US-10-981-356A-25
US-10-981-356A-27
US-10-981-356A-28
US-11-096-046-25
US-11-096-046-28
US-11-096-046-28
US-10-981-356A-26
US-11-096-046-26
US-11-096-046-26
US-11-096-046-26
US-11-096-046-26
US-11-096-046-26
US-10-512-184-71
US-10-512-184-71
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US-11-116-939-12

US-11-116-939-12

US-11-239-510-23

US-11-239-510-13

US-11-239-510-19

US-11-239-10-19
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Publication No. US20050287164A1
GENERAL INFORMATION:
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Sequence 2965, Ap
Sequence 3, Appli
Sequence 3, Appli
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Sequence 1, Appli
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388.792 Million cell updates/sec
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Sequence 1, A
Sequence 29, A
Sequence 29, Sequence 6, A
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                                                                                                                                                                                                                                                                                          1 NIMLTQSPSSLAVSAGEKVT......CHQYLSSRTFGGGTKLEIKR
                                                                                                                                                       May 9, 2006, 01:59:22 ; Search time 13.4524 Seconds
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1: /SIDS5/ptodata/2/pubpaa/US08 NEW PUB.pepl:*
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3: /SIDS5/ptodata/2/pubpaa/US08 NEW PUB.pep:*
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5: /SIDS5/ptodata/2/pubpaa/US08 NEW PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US09 NEW PUB.pep:*
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9: /SIDS5/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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11: /SIDS5/ptodata/2/pubpaa/US11 NEW PUB.pep:*
12: /SIDS5/ptodata/2/pubpaa/US11 NEW PUB.pep:*
                           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-512-184-70
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US-11-219-563-91
US-11-218-813-71
US-11-218-813-91
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US-10-981-356A-1
US-11-096-046-1
US-10-981-356A-29
US-11-136-559-6
US-11-136-559-14
US-11-136-559-12
US-11-136-559-12
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                            Sequence 1, Application US/10981356A
Fublication No. US20060015952A1
GENERAL INFORMATION:
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P206R1
CURRENT APPLICATION NUMBER: US/10/981,356A
FRIOR APPLICATION NUMBER: US 60/520,398
PRIOR PAPLICATION NUMBER: US 60/520,398
PRIOR PLING DATE: 2003-11-13
PRIOR PLING DATE: 2004-03-31
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APPLICANT: PERRARA, NAPOLEONE
APPLICANT: PERRARA, NAPOLEONE
APPLICANT: PERGYP, ELLEN H.
APPLICANT: PRESTA, LEONARD G.
APPLICANT: PRESTA, LEONARD G.
APPLICANT: PRESTA, LEONARD G.
APPLICANT: PERGY, LEONARD G.
TITLE REPERBYCE: P1954R1US
CURRENT PAPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR PERGY BOTTON NUMBER: US 60/558,290
PRIOR APPLICATION NUMBER: US 60/558,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.6%; Score 544; DB 9; Best Local Similarity 92.0%; Pred. No. 2.6e-33; Matches 104; Conservative 6; Mismatches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/11096046 Publication No. US20050276802A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.09
Matches 104; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-1
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RESULT 2
US-10-981-356A-1
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TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT FILLS OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT FILLS OF PRIOR APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398
PRIOR PILLING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR PILLING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%; Score 544; DB 9; Length 666;
92.0%; Pred. No. 1e-32;
tive 6; Mismatches 3; Indels
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APPLICANT: ADAMS, CANELLIA W.
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: MAO, WEIGUANG
APPLICANT: MAO, WEIGUANG
APPLICANT: FILVAROFF, ELLEN H.
APPLICANT: FEJADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
FILE REFERENCE: P1954R1US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Sequence is synthesized US-10-981-356A-29
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CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 29
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; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29
US-10-981-356A-29
. Sequence 29, Application US/10981356A
; Publication No. US2066015952A1
; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Best Local Similarity 92.0%
Matches 104; Conservative
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Best Local Similarity
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
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                                                 SEQ ID NO 14
LENGTH: 112
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                   61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSDFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIK 112
                                                                                                                                                          APPLICANT: PATTI, Joseph M
APPLICANT: PATTI, Joseph M
APPLICANT: DOMANSI, Paul
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSI, Paul
APPLICANT: PATEL, Practisha
APPLICANT: HALL, Andrea
ITILE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P0706940846,
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT APPLICATION NUMBER: US/10/056,052
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
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PRIOR FILING DATE: 2001-03-12
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Publication No. US20050287164A1
GENERAL INFORMATION:
                                                                                                          Sequence 6, Application US/11136559 Publication No. US20050287164A1 GENERAL INFORMATION:
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APPLICANT: PATTI, Joseph M
APPLICANT: PATTI, Joseph M
APPLICANT: PATTI, Joseph M
APPLICANT: PATTI, Joseph M
APPLICANT: PATEL, Pratiksha
APPLICANT: PATEL, MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: PO7069US04/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-03-12
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                                                                                                                    Length 112;
                                                                                                                                                                                 4; Indels
                                                                                                                Query Match
92.1%; Score 535; DB 11;
Best Local Similarity 91.1%; Pred. No. 1.1e-32;
Matches 102; Conservative 6; Mismatches 4;
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TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus aureus
US-11-136-559-22
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SOFTWARE: Patentin versic
SEQ ID NO 22
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Sequence 33, Application US/10512184
Sequence 33, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SSQ ID NO 33
LENGTH: 259
                                                                                                                      Sequence 68, Application US/10512184
Publication No. US20050244901A1
Publication No. US20050244901A1
Publication No. US20050244901A1
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
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198 ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPFTFGSGTKLEIKR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2
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Pred. No. 2.3e-28;
9; Mismatches 10; Indels 1
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Pred. No. 3.8e-29;
9; Mismatches 8
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CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VET. 2.1
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ORGANISM: Artificial Sequence
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Best Local Similarity 82.5%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.6'
Best Local Similarity 84.2'
Matches 96; Conservative
                                                                                                     US-10-512-184-68
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Publication No. US20050244901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: 2011.01051
TURENT APPLICATION NUMBER: US/10/512,184
CURRENT PILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
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                                                               APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REPERENCE: PO70699304/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT APPLICATION NUMBER: US/10/056,052
PRIOR APPLICATION NUMBER: US/10/056,052
PRIOR PRILING DATE: 2002-01-18
PRIOR PLLING DATE: 2001-01-18
PRIOR PLLING DATE: 2001-07-30
PRIOR PLLING DATE: 2001-06-18
SOFTWARE: PACENTIN VOMBER: 60/264,072
PRIOR PLLING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PACENTIN VERSION 3.1
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Pred. No. 3.1e-29;
9; Mismatches 8;
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Pred. No. 2.7e-31;
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84.2%;
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Best Local Similarity 86.6%;
Matches 97; Conservative 1
                      DOMANSKI, Paul
PATEL, Pratiksha
HALL, Andrea
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Matches 96; Conservative
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LENGTH: 259
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                        APPLICANT:
APPLICANT:
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  61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLELK 113
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                                                                                                                                     Score 474.5; DB 1
Pred. No. 2.8e-28;
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Best Local Similarity 82.3%;
Matches 93; Conservative
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US-11-219-563-91
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                                                                     RESULT 13

US-10-512-184-70

US-10-512-184-70

Sequence 70, Application US/10512184

Sequence 70, Application US/10512184

Sequence 70, Mapplication No. US20050244901A1

SEMERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.;

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: resistance against fungi

FILE REFERENCE: 3581.010501

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOSTWARER: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVPFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPFTFGSGTKLEIKR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLS-SRTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPDRPTGSGSGTDFTLTISSVQSEDLAIYYC-HQYLSSRTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising RS - linker - scFv '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MODIFIED ANTIGEN AND USES THEREOF
; TITLE OF INVENTION: WOMBER: US/11/219,563
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT APPLICATION NUMBER: PCT/US04/06586
; PRIOR PILING DATE: 2004-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR PILING DATE: 2003-03-03
; PRIOR PILING DATE: 2003-03-03
; PRIOR PILING DATE: 2003-03-03
; PRIOR SELING DATE: 2003-03-03
; PRIOR SELING DATE: 2003-03-03
; RIOR PILING DATE: 2003-03-03
; RIOR PILING DATE: 2003-03-03
; RIOR PILING DATE: 2003-03-03
; RIOR APPLICATION NUMBER: 10/449,379
; NUMBER OF SEQ ID NOS: 144
; SOGTWARE: FABELSEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.5%; Score 479.5; DB 9; Length 329; Best Local Similarity 82.5%; Pred. No. 2.8e-28; Matches 94; Conservative 9; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.7%; Score 474.5;
82.3%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.3
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-11-219-563-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-512-184-70
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 70
LENGTH: 329
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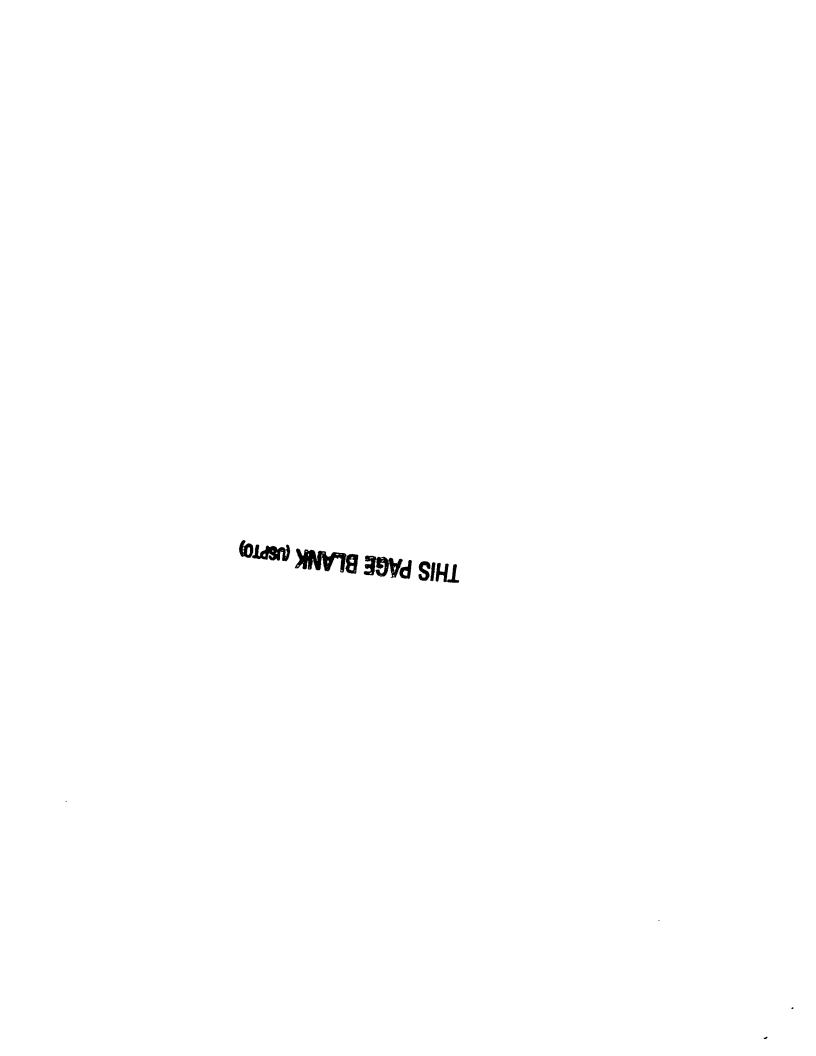
Gaps

1;

10; Indels

Length 113;

DB 10;



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May 9, 2006, 01:18:21; Search time 106.251 Seconds (without alignments) 487.964 Million cell updates/sec
                                                                                                                                                           US-10-700-632-9
623
1 QVQLQQPGAEVVKPGASVKM.......BVRLRYFDVWGQGTTVTVSS 118
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                            2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: genesedp1980
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Perfect score:
Sequence:
                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                            Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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lon	Humanised	Mouse ant	Mouse ant	Chimeric	Chimeric	Mouse ant	Murine an	Murine va	A fusion	B9E9 SCFV	Anti-CD20	Murine an	Mouse ant	Murine im	Murine FU	Protein r	Mature va	Mouse ant	2B8 heavy	Novel chi	Glycoprot	Human CH2	Antibody
Description	Ado32093	Ado32091	Ado32157	Adj94605	Adj 94607	Adj94601	Aao27201	Aar55215	Aab30694	Abj39009	Abr55873	Abu08394	Adc66270	Ade85690	Ade73084	Adf60661	Adn49734	Adu74410	Adv92492	Adv98555	Adz59909	Aae27924	Abb82833
SUMMARIES	AD032093	AD032091	AD032157	ADJ94605	ADJ94607	ADJ94601	AA027201	AAR55215	AAB30694	ABJ39009	ABR55873	ABU08394	ADC66270	ADE85690	ADE73084	ADF60661	ADN49734	ADU74410	ADV92492	ADV98555	ADZ59909	AAE27924	ABB82833
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% Query Match Length DB	118	118	117	121	121	120	123	140	412	412	140	140	140	140	140	140	140	140	140	140	140	360	360
% Query Match	100.0	98.4	97.8	86.4	86.4	85.6	84.9	84.3	84.3	84.3	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2
Score	623	613	609	538.5	538.5	533.5	529	525.5	525.5	525.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5	524.5
Result No.		7	м	4	ιΩ	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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9 ADW77074

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524.5

Ad192472 Antibody Ad192473 Improved Adu68155 Novel var Adu68155 Novel var Adu68154 Novel var Adu68154 Novel var Adv82496 Antibody Adv92496 Antibody Adv98559 Novel chi Adv92500 CD20WH/PC Adv98565 Novel chi Adv92507 CD20WH/PC Adv98565 Novel chi Adv92504 FL/Fc/CD2 Adv98565 Novel chi Adv92504 FL/Fc/CD2 Adv98565 Novel chi Adv92504 FL/Fc/CD2 Adv98565 Novel chi Adv91539 Mature fchi Adv21539 Mature fchi Adv21539 Mature fchi Adv81606 CD3 speci Adz83606 CD3 speci				heavy chain SEQ ID NO:9.	ent; immunoconjugate; cytostatic; myeloid leukaemia; ileukaemia; mouse; humanised;								for treating a disease myelodysplastic syndrome, acute		ed anti-CD33 antibody or its at least one complementarity- heavy chain variable region chain variable region, where so described: (1) an or its epitope-binding fragment sition comprising the antibody or
ADL92472 ADL92473 ADU68155 ADU68154 ADU68154 ADU881832 ADV98559 ADV98563	118 AA.			1y9-6	pe-binding fragment; ng region; CDR; imm! syndrome; acute mye ; pro-myelocytic leu						RJ;		JD33, useful lon, such as	4pp; English.	n isolat ng: (a) at least ne light D33. Als tibody c
<b> </b>					ope- ing s sy			737	332P		Lutz		to ( ress.	24pp	scrill comp comp comp comp comp comp comp comp
4 4 4 4 4 4 4 4 4 6 6 6 6 6 7 4 4 4 4 4	protein			ti-CD33	dy; epitope- determining ysplastic sy leukaemia; p in.			7575505H-0W600C	S-04243	INC.	Ď,		bind 3 exp leuke	9, 1	agment con (CDR); o and at 1 ility to mprising
# # # # # # # # # # # # # # # # # # #	standard:		(£	mouse anti-	ntibody rity-de yelodys loid le y chain	 va vo	4-A2.			UNOGEN	Tavares	-411619/38	tha h CD loid	SEQ ID NO	inventiding fractively fraction 3 CDRs, the abi
2000 2000 2000 2000 2000 2000 2000 200	32093	••	-AUG-2004	Humanised m	anti-CD33 antibody, complementarity-dete antibody; myelodyspl chronic myeloid leuk My9-6; heavy chain.	Mus musculus Homo sapiens Synthetic.	WO200404334	-MAY-2004	-NOV-2002	(IMMU-) IMMUNOGEN INC	Hoffee MG,	WPI; 2004-4	v antibodies sociated wit chronic mye	aim 11; S	The present invention describes a epitope-binding fragment comprisi determining region (CDR); or (b) comprising 3 CDRs, and at least o the CDR has the ability to bind c immunoconjugate comprising the an linked to a drug or prodrug; (2)
0000000000000000044444 000000000000000	SUL 032						-	27	0 6				Nev ass	ជ	
	E A E	×××	FX	X		4888	X 25 X	E X B	XX	<b>A</b>	X II	ž # \$	\$ tt tt tt	X 22 X	88888888

composition comprising the manusconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the defined antibody or antibody fragment is labelled; (5) inhibiting the defined antibody or its epitope-binding fragment; immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its optope-binding fragment that specifically binds to CD33; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment to polynucleotide encoding the antibody or its epitope-binding fragment to defined above; (9) an isolated polynucleotide, (11) a host cell carasformed with the recombinant vector its epitope-binding fragment (10) a recombinant vector comprising the polynucleotide; (11) a host cell cransformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment; (10) chraining CD33 from a biological material. The antibody or its epitope-binding fragment; (10) chraining CD33 from a biological material. The antibody or its epitope-binding fragment; (12) producing a subject having a disease where CD33 from a biological material. The antibody or its epitope-binding fragment, (13) containing CD33 from a biological material. The antibody or its epitope-binding fragment, (13) containing CD33 from a biological material. The antibody or its epitope-binding fragment, (13) containing CD33 from a biological material. The antibody or its epitope-binding containing CD33, and (13) containing cD33, and (13) containing cD33 from a biological material. The present cataining craft or in vivo imaging or as affinity purification agents. The present contains a humanised mouse anti-CD33 antibody My9-6 heavy contains a subject produced and contains a subject produced and contains a subject produced and for invivo unaging or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical nvention 

Sequence 118 AA;

ö 9 9 61 NOKFOCKATLTADKSSTTAYMOLSSLTSEDSAVYYCARBVRLRYFDVWGQGTTVTVSS 118 61 NQKFQGKATLITADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY Gaps ; 0 Length 118; Indels ö 100.0%; Score 623; DB 8; 100.0%; Pred. No. 1.4e-44; iive 0; Mismatches 0; Query Match Best Local Similarity 100.0 Matches 118; Conservative 셤 셤 ሯ ઠ

ADO32091 standard; protein; 118 AA. 12-AUG-2004 AD032091; RESULT 2 AD032091 

(first entry)

Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6; heavy chain.

Mus musculus.

WO2004043344-A2

27-MAY-2004

05-NOV-2003; 2003WO-US032737

07-NOV-2002; 2002US-0424332P

(IMMU-) IMMUNOGEN INC.

Lutz RJ; Tavares D, WPI; 2004-411619/38 Hoffee MG,

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The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the immunoconjugate, composition of the antibody or antibody fragment is labelled; (5) inhibiting the open of antibody or antibody fragment is labelled; (5) inhibiting the open antibody or antibody fragment is labelled; (5) inhibiting the open of antibody or antibody fragment is labelled; (5) inhibiting the open of antibody or its epitope-binding fragment, and a pharmaceutical or or open or its epitope-binding fragment; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment (10) are recombinant vector comprising the ability to bind CD33; and (13) are recombinant vector comprising the ability to bind CD33; and (13) coptaining CD33 from a biological material. The anti-CD33 antibody or its epitope-binding fragment having the ability to bind cD33; and (13) coptaining CD33 from a biological material. The anti-CD33 antibody has correct composition can be used for transiting a subject having a myeloid leukaemia, chroning myeloid leukaemia, chronic m
                                      New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute or chronic myeloid leukemia.
                                                                                                                                                                   Claim 5; SEQ ID NO 7; 124pp; English.
N-PSDB; ADO32140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 118 AA;
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Gaps ; 0 Score 613; DB 8; Length 118; Pred. No. 9.3e-44; 1; Mismatches 1; Indels 98.4%; 98.3%; Best Local Similarity 98.3 Matches 116; Conservative Query Match

QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY

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RESULT 3 AD032157

ADO32157 standard; protein; 117 AA AD032157; 12-AUG-2004 (first entry)

Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.

complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain. anti-CD33 antibody; epitope-binding fragment; 

Mus musculus

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humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb; IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease; thrombocytopenia; lupus; rheumatoid arthritis; heavy chain variable region.
                                                                Chimeric anti-CD20 antibody variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Qu Z, Goldenberg DM;
                                                                                                                                                                                                                                                                                                       L4-FEB-2003; 2003WO-GB000665.
                                                                                                                                                                                                                                                                                                                                      2002US-0356132P.
2002US-0416232P.
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUNOMEDICS INC
(MCCA/) MCCALL J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-697522/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                    WO2003068821-A2
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                                                                                                                                                                                                   Unidentified.
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07-OCT-2002;
                               06-MAY-2004
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 ADJ94605;
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                                                                                                                                                                                     Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least near complementarity—determining region (CDR), or (b) at least heavy chain variable region determining region (CDR), and at least need in variable region, where comprising 3 CDRB, and at least need light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunocollygate comprising the antibody or its epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the immunocollygate, composition or the antibody or the immunocollygate, composition or the antibody or at spitope-binding fragment is labelled; (5) inhibiting the agent; (4) a diagnostic reagent comprising the call with the above defined above, or its epitope-binding fragment is labelled; (5) inhibiting the contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment (7) an improved antibody or its epitope-binding fragment (7) an improved antibody or heavy chain of the antibody or its epitope-binding fragment (7) are combinant vector comprising the polymucleotide encoding the antibody or its epitope-binding fragment (8) are some or its epitope-binding a subject having a subject 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                    New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 609; DB 8; Length 117;
Pred. No. 2e-43;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       Example 3; SEQ ID NO 73; 124pp; English.
                                                                                                                                                                  Lutz RJ;
                                                                05-NOV-2003; 2003WO-US032737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%;
98.3%;
                                                                                                07-NOV-2002; 2002US-0424332P
                                                                                                                                                                                                                                                                      or chronic myeloid leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115; Conservative
                                                                                                                                                                    Tavares D,
                                                                                                                                 (IMMU-) IMMUNOGEN INC
                                                                                                                                                                                                   WPI; 2004-411619/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 AA;
WO2004043344-A2.
                               27-MAY-2004
                                                                                                                                                                  Hoffee MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nvention.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAb) or its antigen-binding fragment containing the complementarity determining regions (CDRs) of at least one murine anti-CD20 Mab variable region and the framework regions (FRs) of at least one human IVIAB variable region. The antibodies of the invention are useful for diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The present amino acid sequence represents a chimeric anti-CD20 antibody
New humanized anti-CD20 monoclonal antibody (MAb) that retains ubstrantially the B-cell and B-cell lymphoma and leukemia cell targeting of the murine anti-CD20 MAb, useful for treating B-cell lymphoma, leukemia or an autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                  invention comprises a humanised anti-CD20 (hCD20)monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.4%; Score 538.5; DB 7; Length 121; 84.3%; Pred. No. 1.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                        Disclosure; Fig 2B; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ94607 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ94607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ94607
ID ADJ9
XX
AC ADJS
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ADJ94605 standard; protein; 121 AA

ADJ94605 ID ADJ9 XX RESULT

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14-FEB-2002; 2002US-0356132P. 07-OCT-2002; 2002US-0416232P.
                                                                                                                                                                                                                     Goldenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.6%;
84.2%;
                                                                                                                                 14-FEB-2003; 2003WO-GB000665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 101; Conservative
                                                                                                                                                                                     (IMMU-) IMMUNOMEDICS INC. (MCCA/) MCCALL J D.
                                                                                                                                                                                                                                           WPI; 2003-697522/66.
N-PSDB; ADJ94600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120 AA;
                                                                                     WO2003068821-A2
                                                                                                           21-AUG-2003
                                                                                                                                                                                                                      Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA027201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKFKGKATLTADKSSSTAYMOLSSLTSEDSAVYYCARSTYYGGDWYFDVWGQGTTVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                  (MAb) or its antigen-binding fragment containing the complementarity determining regions (CDRs) of at least one murine anti-CD20 Mab variable region and the framework regions (FRs) of at least one human IVIAB variable region. The antibodies of the invention are useful for diagnosing or preventing B-cell lymphoma. Jeukaemia or an autoimmune disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The present amino acid sequence represents a chimeric anti-CD20 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                            New humanized anti-CD20 monoclonal antibody (MAb) that retains substantially the B-cell and B-cell lymphoma and leukemia cell targeting of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                       humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb; IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease; thrombocytopenia; lupus; rheumatoid arthritis; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a humanised anti-CD20 (hCD20)monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 538.5; DB 7;
Pred. No. 1.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse anti-CD20 antibody variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                              leukemia or an autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ94601 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Fig 4A; 106pp; English.
                                                                                                                                                                                                                                                                 Goldenberg DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
                                                                                                                                                                                                  14-FBB-2002; 2002US-0356132P, 07-OCT-2002; 2002US-0416232P.
                                                                                                                                                                            14-FEB-2003; 2003WO-GB000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                                                                 (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variable heavy chain.
                                                                                                                                                                                                                                                                                       WPI; 2003-697522/66.
                                                                                                                                                                                                                                             (MCCA/) MCCALL J D.
                                                                                                                                                                                                                                                                 g 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 121 AA;
                                                                                                                                 WO2003068821-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S 121
                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
06-MAY-2004
                                                                                                                                                       21-AUG-2003
                                                                                                                                                                                                                                                                 Напвеп Н,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ94601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ94601
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셤
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(MAb)or its antigen-binding fragment containing the complementarity determining regions (CDRs) of at least one murine anti-CD20 Mab variable region and the framework regions (FRs) of at least one human IVIAB variable region. The antibodies of the invention are useful for diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune grease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The present amino acid sequence represents a mouse anti-CD20 antibody variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention comprises a humanised anti-CD20 (hCD20)monoclonal antibody
humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
thrombocytopenia; lupus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-CD20 monoclonal antibody (MAb) that retains substantially the B-cell and B-cell lymphoma and leukemia cell ta of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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Pred. No. 4.3e-37;
7; Mismatches 9; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine anti-CD20 antibody, 1F5, VH protein.
                                                                                                                    heavy chain variable region; mouse; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukemia or an autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA027201 standard; protein; 123 AA
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us-10-700-632-9.rag

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Treating B cell lymphoma with chimeric antibody - against CD20, causing rapid depletion of peripheral B cells, also new antibodies and
                                                                                             cell lymphoma chimeric antibody; CD20; peripheral blood cells;
                                                               Murine variable region heavy chain from 2BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 101pp; English.
                                                                                                                                                                                                                                      93WO-US010953.
                                                                                                                                                                                                                                                                    92US-00978891.
                                                                                                                                                                                                                                                                                                                                              Anderson DR, Rastetter WH,
Reff ME;
                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                  (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-183162/22.
N-PSDB; AAQ65631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 140 AA;
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                                                                                                                                           Mus musculus.
                                                                                                                                                                          WO9411026-A2
                  25-MAR-2003
01-FEB-1995
                                                                                                                                                                                                                                      12-NOV-1993;
                                                                                                                                                                                                                                                                    13-NOV-1992;
03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-2001
                                                                                                                                                                                                         26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridomās.
                                                                                                            cell lysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on 25-MAR-;
PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel re-engineered or framework (FR)-patched immunoglobulin, containing the heavy and/or light chain variable region (WH/WL) sequences from a parent antibody. Within these chains, at least cone of the compartmentalised framework sequences, defined as FR1, FR2, FR3 and FR4 are replaced, or patched, by the corresponding framework sequences from the heavy and light chain immunoglobulin region of a different species. The FR-patched immunoglobulin binds specifically to an artigen with affinity comparable to, or within 3-fold of, that of the parent immunoglobulin. The invention discloses the process of FR-patching which is used to generate re-engineered immunoglobulin chains having one or more complementarity determining regions (CDK's) from a donor immunoglobulin and portions of framework sequences from one or more human or portions of framework sequences from or or more human or portions of framework sequences from or or more complementarity determining regions (CDK's) from a donor immunoglobulin and portions of framework sequences from or or more complementarity determining regions (CDK's) from a donor complementarity as well as reduced or eliminated immunogenicity, whilst maintaining the specificity and affinity of the parent antibody. The FR-patched immunoglobulin is useful during the preparation of a composition of the treatment of rheumatoid arthritis. Furthermore, the molecules of the invention may also prove useful in gene therapy. The current sequence is that of the murine anti-CDSO antibody, 1F5, WH protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                               New re-engineered or framework-patched immunoglobulin, useful for preparing a composition for treating cancer, preferably Non-Hodgkin's lymphoma or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLRQPGAELVKPGASVRMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYPGNGDTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .66 .
te= "Complementarity determining region (CDR) 2"
                                                                                           Ę
                               "Complementarity determining region (CDR) 1"
                                                                                             (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ;
                                                              /note= "Complementarity determining region
99. .111
/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 84.9%; Score 529; DB 6; Length 123; Local Similarity 82.0%; Pred. No. 1.1e-36; Length 10; Conservative 9; Mismatches 9; Indels
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 7a; 66pp; English
                                                                                                                                                                                       10-JUN-2002; 2002WO-US018512
                                                                                                                                                                                                                    27-JUN-2001; 2001US-00892613
                                                                                                                                                                                                                                                                                                                WPI; 2003-210245/20.
                                                                                                                                                                                                                                                  (LEUN/) LEUNG S S.
                                                                                                                          WO2003002607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS 122
                                                                                                                                                         09-JAN-2003
                                                                                                                                                                                                                                                                                   Leung SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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 Key
Domain
                                             Domain
                                                                            Domain
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Matches
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Newman RA;

Leonard JE,

Hanna N,

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                                                                                                                                                                                                                                                                                                                              80 NQKFKGKATLIADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDSYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                         61 NOKFOGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRL---RYFDVWGQGTTVTVS 117
The sequence is the murine variable region heavy chain derived from murine anti-CD20 monoclonal antibody 2BS. See also AAQ65629-35. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79
                                                                                                                                                                                                                        1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     3;
                                                                                                                                             DB 2; Length 140;
                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A fusion of anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour cell; cancer; adenocarcinoma; malignancy; B9E9.
                                                                                                                                           Score 525.5; DB 2
Pred. No. 2.4e-36;
9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB30694 standard; protein; 412 AA.
                                                                                                                                             84.3%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                   99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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AAR55215 standard; protein; 140 AA.

**AAR**55215

AAR55215

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Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scFvSA; anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy; cell-specific targeting agents; single chain; tumour; B9E9.
                                                                                                                                                               B9E9 scFvSA fusion protein A amino acid sequence.
                                                            ABJ39009 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2001; 2001US-00013173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2002; 2002WO-US039429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2002; 2002US-00150762
16-SEP-2002; 2002US-00244821
                                                                                                                                                                                                                                                                Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003050260-A2.
                                                                                                                              09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2003.
                                                                                                                                                                                                                                                                                     Mus sp.
Synthetic.
                                                                                               ABJ39009;
                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                             RESULT 10
                                                ABJ39009
                                                                                             The present sequence represents a fusion of an anti-CD20 single chain antibody (B9EB) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid, caricalar. The fusion proteins are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapequeic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumor cells associated with cancer, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTTVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYXIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                     Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 525.5; DB 4; Length 412;
Pred. No. 7e-36;
7; Mismatches 8; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                    Lin Y, Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                  Schultz JE,
                                                                                                                                                                                                /note= "streptavidin"
                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 11B; 100pp; English.
                                                            "VL chain"
                                                                                                                              "VH chain"
                                                                                                                                                             /note= "linker"
254. .412
                                                                                             "linker"
                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000WO-US015595.
                                                                                                                                                                                                                                                                                                                                  99US-0137900P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.6%;
Matches 102; Conservative
                                                                                                              . 248
                                                                                                                                               . 253
                                                .108
                                                                              109. .17
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                     Graves SS,
                                                                                                                            /note=
249. .2
                                                            'note=
                                                                                                                127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                    (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC86563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenocarcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS 248
                                                                                                                                                                                                                                 WO200075333-A1.
Ното варіепв.
                                                                                                                                                                                                                                                                                                                                  07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                03-DEC-1999;
                                                                                                                                                                                                                                                                  14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    Goshorn SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                             Protein
                                                                              Peptide
                                                                                                              Protein
                                                                                                                                                                               Protein
                                                                                                                                               Peptide
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/note= "Streptavidin region of the fusion protein"

248. 253 /note= "Synthetic linker region" 254. 412

protein"

'note= "VL region of the fusion protein" 107. .127

Location/Qualifiers

(first entry)

'note= "Synthetic linker region (pKOD)"

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This invention relates to novel vector constructs for the expression of streptavidin fusion proteins. Streptavidin (SA) is produced by Streptavidin fusion proteins. Streptavidin (SA) is produced by vectors avidinia and specifically binds water-soluble biotin. The vectors comprise a nucleic acid sequence encoding streptavidin, a promoter operatively linked to the nucleic acid sequence and a cloning site for insertion of a second nucleic acid sequence encoding an antience of the antigen binding fragment. The fusion proteins encoded are known as single chain antibody-genomic streptavidin fusion proteins (scFvSA). The vectors may have cytostatic activity when used in streptavidin fusion cassettes. The fusion proteins may be used as diagnostic markers or as cell-specific targeting agents. These may also be used in treating tumours. The present sequence is the amino acid sequence of the BPS9 single chain antibody-genomic streptavidin fusion
                                                                                                                                                                                                                                                                                                                                                             New vector construct for expressing genomic streptavidin fusion proteins useful as diagnostic markers or as cell-specific targeting agents.
                                                                                       Schultz JE, Lin Y, Sanderson JA, Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11B; 156pp; English,
                                                                                            Graves SS,
                                                                                                                                                                                                                               WPI; 2003-532908/50.
N-PSDB; ABT43498.
(NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 412 AA;
                                                                                       Goshorn SC,
Dearstyne EA;
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peptide, interjeuring (IL.2) peptide, Factor VIII peptide, TRFalpha, receptor/immunoglobulin (1g) G fusion peptide, urokinase peptide, antiglycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2 antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-nulin peptide, hepatitis B surface antigen (Hbsag), human growth hormone (HGH) peptide, and a modifying group, where the modifying group is covalently attached to the peptide through an intact glycosyl linking group. The method is useful for a cell-free, in vitro method of remodeling the above mentioned peptides. The present sequence represents the murine anti-CD20 antibody heavy chain mature variable region
                                                                                                                                                                                                                                                                                                                                                   61 NOKPOCKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                80 NOKFKGKATLTADKSSSTAYMOLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating B cell lymphoma in humans, comprises administering immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled anti-CD20 antibodies to the human.
                                                                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                          1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
    beta-glucosidase peptide, tissue plasminogen activator (TPA)
                                                                                                                                                                                                                            Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20. .140 ____/label= Mature_anti-CD20_antibody_VH_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; expression vector; murine; heavy chain; variable region.
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reff MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine anti-CD20 antibody heavy chain variable region.
                                                                                                                                                                                                                              Score 524.5; DB 6;
Pred. No. 2.9e-36;
9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU08394 standard; protein; 140 AA.
                                                                                                                                                                                                                            / Match
Local Similarity 81.8%;
les 99; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2001; 2001US-00911703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00475813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-352746/33.
N-PSDB; ABX94209.
                                                                                                                                                                                                  Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002197255-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                          140 A 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson DR,
Rastetter WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU08394;
                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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Matches
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                                                                                         187
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C
                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                            remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycan, and contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl donor to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSF) peptide, interferon alpha peptide, interferon beta peptide, Factor VI a peptide, follicle stimulating hormone peptide, erythropoietin (EPO) peptide, granulocyte macrophage colony stimulating factor (G-CSF) peptide, peptide, granulocyte macrophage colony stimulating factor (G-CSF) peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remodeling a peptide, by removing a saccharyl subunit from the peptide form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the
                                                                              NOKFOCKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTTVTV
                                                                                                                                                   NOKFKGKATLITADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTV
                                                           QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                Gaps
                                5,
   DB 6; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen X;
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hakes
84.3%; Score 525.5; DB
83.6%; Pred. No. 7e-36;
ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bowe C,
                                                                                                                                                                                                                                                                                      ABRS5873 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 83B; 900pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0387292P.
2002US-0391777P.
2002US-0396594P.
2002US-0404249P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0344692P.
2001US-0334233P.
2001US-0334301P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2002; 2002WO-US032263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0328523P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0407527P
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zopf D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-449162/42.
N-PSDB; ACC78895.
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003031464-A2.
                                                                                                                                                                                 SS 118
                                                                                                                                                                                                             SS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2002;
16-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Frees S,
                                                                                                                                                                                                                                                                                                                                                  02-SEP-2003
                             102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2003
                                                                                                                                                                                                                                                                                                                    ABR55873;
                                                           -
                                                                                                                                                 188
                                                                                                                   61
                                                                                                                                                                                                             247
 Query Match
                                                                                                                                                                               117
                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                             Matches
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9 79

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The invention relates to an improved method for treating B cell lymphoma comprising administering an anti-CD20 antibody. The improvement comprises administering at least one chemotherapeutic agent. The antibody causes a substantial depletion of peripheral B cells. The antibody is chimeric anti-CD20 or C2B8. The method is useful for treating B cell lymphoma. This sequence represents a murine immunoglobulin heavy chain variable region used in the method of the invention.
bonded to the N-acetylglucosamine residue at the reducing end of the usugar chain. The calls are used in the treatment and prevention of cancer and immune disorders. This sequence corresponds to a protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                      61 NOKFOCKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR---YFDVWGOGTTVTVS 117
                                                                                                                                                                                                                                                                                                                           80 NQKFKGKATLITADKSSSTAYMQLSSLISEDSAVYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating B cell lymphoma by administering an anti-CD20 antibody and at least one chemotherapeutic agent.
                                                                                                                                                                                                                                                1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                              7; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 524.5; DB 7; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B cell lymphoma; anti-CD20; peripheral B cell; C2B8; immunoglobulin heavy chain variable region; mouse; antibody.
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine immunoglobulin heavy chain variable region.
                                                                                                                                         84.2%; Score 524.5; DB 7;
81.8%; Pred. No. 2.9e-36;
ive 9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leonard JE, Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example, SEQ ID NO 11; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE85690 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-2002; 2002US-00238681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00978891.
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                                                                                                                                                              Local Similarity 81.8
hes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IDEC-) IDEC PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-897520/82.
N-PSDB; ADE85689.
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                                                                                                        Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                      S 118
                                                                                                                                                                                                                                                                                                                                                                                                                             A 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DR,
Rastetter WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1993;
29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                NOKFOGKATLIADKSSTIAYMOLSSLISEDSAVYYCAREVRLR---YFDVWGQGTIVIVS 117
                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                         79
                                   The present invention relates to a method for treating B cell lymphoma. The method comprises administering at a first administration period, an immunologically active, mouse/human chimeric anti-CD20 antibody and/or administering, at a second administration period, a radiolabelled anti-CD20 antibody, to the human subject. The invention also discloses expression vectors that may be used in the method of the present invention. The method is useful for treating B cell lymphoma in humans. The present sequence represents murine anti-CD20 antibody heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to cells producing an antibody molecule specifically binding to CD20 are new, in which the antibody contains N-glycoside bond complex sugar chains bonded to the Fc region of the antibody peptide chains, of which less than 20% have a fucose residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody binding to CD20 and having Fc-bound sugar chains of low fucose content for treatment of cancer and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLQQPGABLVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressant; cytostatic; antibody; CD20; N-acetylglucosamine; sugar chain; fucose; N-acetylglucosamine; sugar chain; cancer; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakano
                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                      Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Satoh M,
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse anti-CD20 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinkawa T,
                                                                                                                                                                                                                                                                                      Score 524.5; DB 6
Pred. No. 2.9e-36;
9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 14; 200pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC66270 standard; protein; 140
  5; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-DEC-2001; 2001JP-00392753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-DEC-2002; 2002WO-JP013534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002; 2002JP-00106948
01-NOV-2002; 2002JP-00319975
                                                                                                                                                                                                                                                                                      84.2%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shitara K, Sakurada M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADC66269
                                                                                                                                                                                                                                              Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003055993-A1.
                                                                                                                                                                                                      variable region
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  Example, Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
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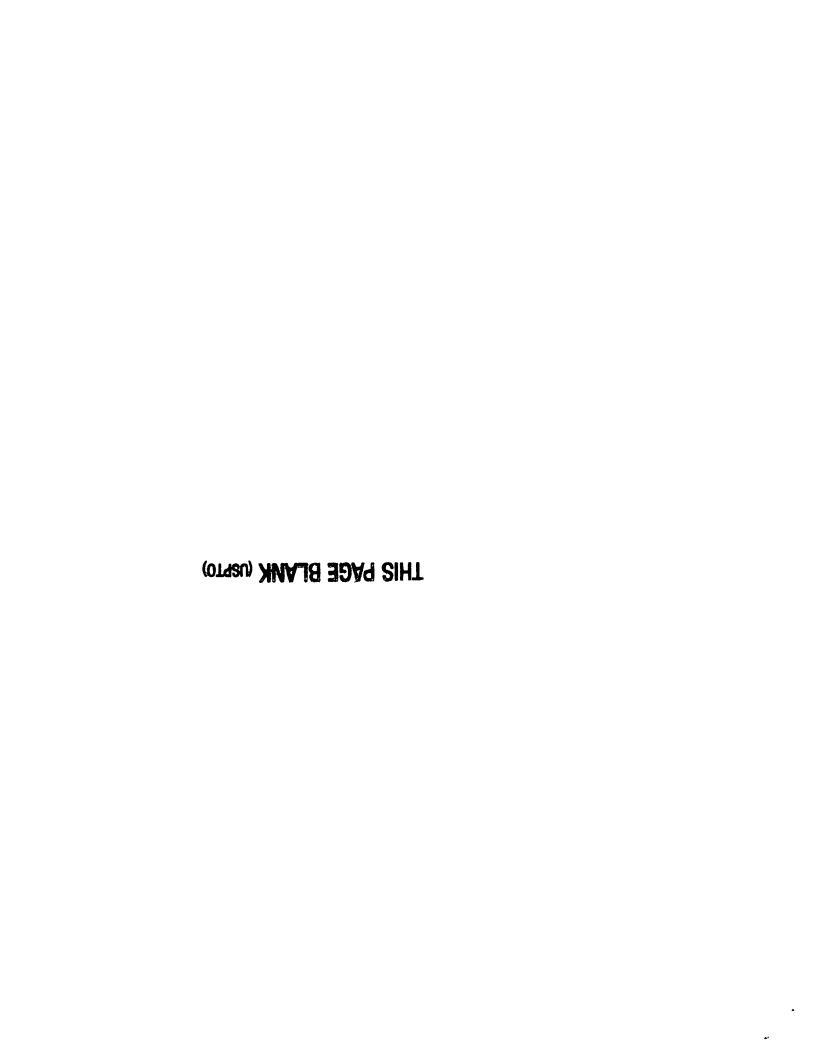
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modifying enzyme activity. The enzyme activity of binding the 1-position of fucose to the 6-position of an N-acetylglucosamine at the reducing end of a complex N-glycoside linked sugar chain via an alpha-bond is absent or less than in the parent cell. The sugar chain modifying enzyme is preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-ADE73055). The invention is useful for the treatment and prevention of tumours, allergy, inflammation, autoimmune disease, criculatory disorders, and viral and bacterial infection. The present sequence was
                                                                                                                                                80 NQKFKGKATLTADKSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                           61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                                         9
                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cells with reduced or absent alpha 1,6-fucosyltransferase activity for treatment of tumors, allergy, inflammation, autoimmune disease, circulatory disorders, and viral and bacterial infection.
                                                                          20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                    3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial; Antivizal; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour; allergy; inflammation; autoimmune disease; circulatory disorder; viral infection; bacterial infection; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to cells with modified sugar chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 140; Score 524.5; DB 7; Length 140; 112 11.8%; Pred. No. 2.9e-36; Conservative 9; Mismatches 10; Indels 3
                   10; Indels
81.8%; Pred. No. 2.9e-36;
tive 9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 165-166; 187pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamano K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in an example from the invention
                                                                                                                                                                                                                                                                                                                                ADE73084 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine FUT8-related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2003; 2003WO-JP004507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamane N, Satoh M, Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2002; 2002JP-00106953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
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                 99; Conservative
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Best Local Similarity
Matches 99; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-833570/77.
 Best Local Similarity
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                                                                                                                                                                                                                                      140 A 140
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                 Matches
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1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY

3;

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61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                                                                     80 NOKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79
                                                                                                                                                                                                                                             Search completed: May 9, 2006, 01:25:27
Job time : 107.251 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

9, 2006, 01:25:51; Search time 17.8788 Seconds (without alignments) 635.031 Million cell updates/sec May Run on:

US-10-700-632-9 623 1 QVQLQQPGAEVVKPGASVKM......EVRLRYFDVWGQGTTVTVSS 118 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR 80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SOFTWARES	Ħ	B22769	PL0089	2 S38717 Ig heavy chain V r	E32513	825175		S21810	G28195	A54378	S42184	S42179	S42180	2 S66537 Ig heavy chain V r	MHMSJ5	S20646	. MHMS18 Ig heavy chain pre		853751	F28195	A30577 Ig heavy	PC1155 Ig heavy chain	G2MS43 Ig heavy chain	S38950 Ig gamma chain	S40295 Ig	S41394 Ig	A39276 Ig heavy	MHMS4E Ig heavy chain	TO1407	TOTAO,
	Length DB	! !					136	•								•	139	287 4						246 2				117 1		
oje	Query	79.6	78.1	78.0	77.6	77.4		7.	76.7	9.94	75.8	75.8	75.8	75.6	75.5	75.5	75.4	75.4	75.1	75.1	75.1	75.0	75.0	74.9	74.9		74.8	74.6	3 76	
	Score	496	486.5	486			482.5	479.5	478	477	472	472	472	471	470.5	470.5	470	470	468	468	468	467	467	466.5	466.5	466	466	464.5	7 77	ř
	Result No.	-	71	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	2

heavy chain	heavy	heavy chain	heavy chain	Ig heavy chain V r	heavy chain	heavy	heavy chain	heavy	heavy	_					
JL0076	PL0238	PH1482	PH1484	A27609	S20640	A24672	F29380	803305	S38565	S55542	S55541	MHMS15	PS0024	PH1489	S25176
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141	115	140	140	139	119	119	137	117	118	116	117	120	139	140	117
	8.	73.8	73.6	73.5	73.4	73.4	73.4	73.3	73.3	73.1	72.9	72.9	72.9	72.8	72.7
74.2	7														
~	460 73		458.5	458	457.5	457	457	456.5	456.5	455.5	454	454	454	453.5	453

## ALIGNMENTS

RESULT 1 B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C;Accession: B22769
R;Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A; Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A;Reference number: A90971; MUID:84236026; PMID:7188353
A;Accession: B22769
A;Molecule type: protein
A;Residues: 1-120 <dil></dil>
A;Cross-references: UNIPARC:UP10000176B76
A/Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2
A;Note: peptides and unsequenced residues were positioned by homology with the B1-8 seqn
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>

Gaps 5, Query Match 79.6%; Score 496; DB 2; Length 120; Best Local Similarity 77.5%; Pred. No. 2.5e-37; Matches 93; Conservative 12; Mismatches 13; Indels

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61 NOKFOGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAR--EVRLRYFDVWGQGTTVTVSS 118 9 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY a ઠે ઠ

61 NQKFKGKATLITVDKPSSTAYMQLSSLITSEDSAVYYCARYDYYGSSYFDYWGQGTTLITVSS 120 셤

RESULT 2. PL0089

Pubuses
Figures
Figure

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C;Accession: S25175
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
A;Description: Structure and binding properties of monoclonal antibodies to core histone A;Reference number: S25174
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP100001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID C;Superfeanily: immunoglobulin V region; immunoglobulin homology C;Koywords: heterotetramer; immunoglobulin C;Koywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: PL0208
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reactin. A;Reference number: PL0207; MUID:90309764; PMID:1973259
A;Accession: PL0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c) C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
80 NEKFKSKATLTVDTSSSTAYMQLSSLTSDDSAVYYCARRL-YRYYAMDYWGQGTSVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFOGKATLITADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVQLQQPGSELVRPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGNIYPGSGDSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGQGLEWIGNIDPSDSETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFOCKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGQGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 120;
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A, Cross-references: UNIPARC; UPI0000176C6F
A, Experimental Bource: hybridoma cell E225
c, Superfamily: immunoglobulin V region; immunoglobulin |
F;1-19/Domain: signal sequence #status predicted <SIG>F;1-117/Domain: immunoglobulin homology <IMM>F;36-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.4%; Score 482.5; DB 2; 75.8%; Pred. No. 4e-36; ive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.4%; Score 482.5; DB 2 74.6%; Pred. No. 4.6e-36; ative 17; Mismatches 12.
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nes 91; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <MON>
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                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: 838717
Submitted to the EMBL Data Library, November 1993
A;Reference number: 838713
A;Reference number: 838713
A;Reference number: 838713
A;Retaus: preliminary
A;Molecule type: mRNA
A;Retaus: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <CIM>A;Residues: UNIPARC:UPI0000117541; EMBL:X76020; NID:g416099; PIDN:CAA53607.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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                                                                                                          1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                   1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                        Length 119;
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                        DB 2;
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                                             1.8e-36;
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                    78.1%; Score 486.5; I 77.3%; Pred. No. 1.8e- ive 11; Mismatches
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                                        Local Similarity 77.3% nes 92; Conservative
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Matches 91; Conservative
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Matches 91; Conserv
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                        Query Match
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A; Residues: 1-115 cAGA.
A; Residues: 1-115 cAGA.
A; Residues: 1-115 cAGA.
A; Cross-references: UNIPARC:UP10000176E3F; GB:568981; NID:9545744; PIDN:AAB30095.1; PID A; Cross-references: UNIPARC:UP10000176E3F; GB:568981; NID:9545744; PIDN:AAB30095.1; PID A; Experimental source: spleen and myeloma cell line MOPC 315.43
A; Note: sequence inconsistent with nucleotide translation A; Note: sequence extracted from NCB1 backbone (NCBIN:144172, NCBIP:144173)
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
A; Reference number: A54378; MUID: 94165109; PMID: 7509814
                                                                                                                                                                                                                                                                                                                                                                                   76.6%;
75.7%;
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89.7%;
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Best Local Similarity 75.7%
Matches 87; Conservative
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Best Local Similarity
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                                 A; Accession: A54378
A; Status: preliminary
A; Molecule type: mRNA
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                                                                                                       C;Accession: S21810
R;Ostermeyer, M; Brack, C.H.; Traunecker, A.; Koehler, G.
R;Ostermeyer, M; Brack, C.H.; Traunecker, A.; Koehler, G.
R;Ostermeyer, M; Brack, C.H.; Traunecker, A.; Koehler, G.
R;Ostermeyer, M; Brack, C.H.; Traunecker, J991
A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha
A;Reference number: S21810
A;Accession: S21810
A;Accession: S21810
A;Accession: S21810
A;Accession: S21810
A;Accession: S1818
A;Mesidues: DNA
A;Residues: DNA
A;Residues: UNIPARC:UPI0000115ED6; EMBL:X56936; NID:G54163; PIDN:CAA40257.1; PID
C;Genetica:
C;Genetica:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;34-117/Domain: immunoglobulin homology <IMM>
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R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresd
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C; Species: Whe musculus (house mouse)
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C; Accession: G28195
A; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A; Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid 6
A; Reference number: A28195; MUID:88153717; PMID:3267217
A; Residues: 1-120 <-SHE>
A; Residues: 1-120 <-SHE>
A; Residues: 1-120 <-SHE>
A; Residues: Internet immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <-IMM>
F; 15-98/Domain: immunoglobulin homology <-IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOKFOGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRY-FDVWGOGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                           Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region anti-triplex DNA - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.0%; Score 479.5; DB 2
Best Local Similarity 76.5%; Pred. No. 8.6e-36;
Matches 91; Conservative 11; Mismatches 16
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nes 91; Conserv
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Best Local S:
Matches 91
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Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: 842179
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spectate number: 842176; MUID:94009207; PMID:7691608
A;Accession: S42179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPARC:UP1000011655F; EMBL:Z25447; NID:g407816; PIDN:CAA80934.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B cells with spec
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                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dace: 28-58-59-1994 #sequence_revision 21-Jul-1995 #text_change 06-Jun-1997
C;Accession: 542184
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cel
A;Reference number: 542176; MUID:94009207; PMID:7691608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLOOPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISYN
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                                                                                                                                               1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                       Gaps
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                                                                                                                                                                                                                           61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Length 115;
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A;Residues: 1-101 <MOJ>
A;Croserreferences: UNIPARC:UPI0000176E59; EMBL:225457
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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; DB 2;
1.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 472; DB 2;
Pred. No. 2.9e-35;
6; Mismatches 4;
                                                    13; Mismatches
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Score 477;
                             Pred. No.
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C;Accession: A26242
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
Rature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A;Reference number: A26242; MUID:80078170; PMID:6765983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: 820646
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
R;Losman, M.; Fasy, T.M.; Novick, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S20646
A;Status: preliminary
A;Molecule type: DNA
A;Rebidues: 1-123 cLOS>
A;Cross-references: UNIPARC:UPI0000116020; EMBL:X65001; NID:952612; PIDN:CAA46134.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
                                                                                           61 NEKFKGKATLISDKSSSTAYMELSSLISEDSAVYYCARDYRYDWYYAMDYWGQGTTVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDV------WGQGT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFOCKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKGKATLITVDKSSSTAYMQLNSLISEDSAVYYCARD-RYWYFDVWGAGTITVTVSS 117
                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
        1 EVKLQESGAGLVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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A;Residues: 1-117 <SCH>
A;Cross-references: UNIPROT:P01757; UNIPARC:UP100000270F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.5%; Score 470.5; DB 1 76.3%; Pred. No. 4.6e-35;
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Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local
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S66537
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S66536
R;Tsiotis, G; Haase, W; Engel, A.; Michel, H.
Bur. J. Blochem. 231, 823-830, 1995
A;Title: Isolation and structural characterization of trimeric cyanobacterial photosyste
A;Reference number: S66537
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <TSI>A;Accession: S66537
A;Residues: 1-131 <TSI>A;Residues: UNIPARC:UPI00001137AF; EMBL:X88902; NID:g8995869; PIDN:CAA61364.1; PI
C;Superfenni: immunoglobulin vegion; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <INM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: 842180
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Bur. J. Immunol. 23, 2563-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spect A;Reference number: 842176; MUID:94009207; PMID:7691608
A;Accession: S42180
A;Accession: July Amologopy; Amologopy
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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                                                                                                               Length 101;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin P;15-98/Domain: immunoglobulin homology <1MM>
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ilarity 73.8%; Pred. No. 4.7e-35;
Conservative 15; Mismatches 13.
                                                                                                               Score 472; DB 2;
Pred. No. 2.9e-35;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.8%; Score 472; DB 2; Best Local Similarity 89.7%; Pred. No. 2.9e-35; Matches 87; Conservative 6; Mismatches 4
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89.7%;
                                                                                                         Query Match
Best Local Similarity 89.73
Matches 87; Conservative
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Best Local Similarity
Matches 90; Conserv
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<sup>113</sup> TVTVSS 118 :||||| 118 SVTVSS 123

Search completed: May 9, 2006, 01:33:50 Job time : 17.8788 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Minimum DB Maximum DB

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01-DEC-2001 (TERMELRE1. 19, Last sequence update)
01-DEC-2001 (TERMELRE1. 19, Last sequence update)
01-MAR-2004 (TERMELRE1. 26, Last annotation update)
Name-V165-D-J-C mu;
Name-V165-D-J-C mu;
Mammallas (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Murridae; Murinae; Mus.
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091067,
091067,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2005 (TrEMBLrel. 29, Last sequence update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
VH186.2-D-J-C mu protein (V304-D-J-C mu protein)
Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069915; BAB63931.1; -; mRNA.
PIR; PH1159; PH1159.
HSSP; P01751; IA6W.
SWR; Q924Q0; 1-134.
Ensembl; RNSMUSG0000021155; Mus musculus.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR00110; Ig-11ke.
InterPro; IGV0110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 79.5%; Score 495; DB 2; Similarity 78.0%; Pred. No. 4.9e-45; 92; Conservative 11; Mismatches 15;
             044VABE_MOUSE
0924RI_MOUSE
0924R2_MOUSE
0924R2_MOUSE
0924R1_MOUSE
091WTI_MOUSE
HVO3 MOUSE
0924F7 MOUSE
0924R4_MOUSE
                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                           Q9QXE9_MOUSE
Q924Q2_MOUSE
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 NUCLEOTIDE SEQUENCE
STRAIN=C57BL/6;
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1 QVQLQQPGAEVVKPGASVKM......EVRLRYFDVWGQGTTVTVSS
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(c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
Gamma heavy chain variable region (Fragment).
Name=1gG1 anti-TS1 VH;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
SElandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
Studies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaT81.";
[2] Mol. Recognit. 16:157-163(2003)
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murines, Mus.
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78.0%; Pred. No. 1.7e-44;
iive 11; Mismatches 15; Indels
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                                                                                                                                                                                                          Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069912; BAB63928.1; -; mRNA.
EMBL; AB069914; BAB63930.1; -; mRNA.
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SMR; Q91V67; 1-129.
Ensembl; ENSMGSG00000011155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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les 92, Conservative
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NCBI_TaxID=10090;
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120 AA;
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OSPZII MOUSE
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                                                                                                                              61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRY---FDVWGQGTTVTVS
                                                                                                    1 OVOLOOPGAEVVKPGASVKMSCKASGYTPTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3135311;
Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
"Allogeneic manipulation of the GAT idiotypic cascade. Immunization (C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strainspecific V genes as the original antigen.";
J. Immunol. 141:779-784 (1988).
EMBL, AB667795; BAB63280.1; -; mRNA.
                                                      3;
  Score 488.5; DB 2; Length 120;
Pred. No. 2e-44;
9; Mismatches 13; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sec
01-OCT-2003 (TrEMBLrel. 25, Last ann
VH186.2-D-J-C mu protein (Fragment)
Mame-VH186.2-D-J-C mu;
Mus musculus (Mouse).
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: 15908 MW; 5
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 1
       78.4%;
79.2%;
Query Match
Best Local Similarity 79.2°
Matches 95, Conservative
                                                                                                                                                                                                                                                                                                                                                                          Q924Q5_MOUSE PRELIMINARY;
Q924Q5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH1105.
PH1108.
PH1114.
PH1118.
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PH1128.
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PH1153; PH1153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; PH1153; PH115.
HSSP; P01751; 1A6W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMR; Q924Q5; 1-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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PH1108;
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PH1118;
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PH1125;
PH1126;
PH1128;
PH1129;
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PH1150;
PH1151;
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PH1137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PH1142;
PH1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PH1131;
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NON TER
SEQUENCE
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Gaps

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Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;

A Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;

T Allogeneic manipulation of the GAT idiotypic cascade. Immunization of C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
T Specific V genes as the original antigen.";

J. Immunol. 141:779-784(1988).

R BRB., AB66781; BA863266.1; -; mRNA.

R PIR; PH1105; PH1106.

R PIR; PH1114; PH1114.

R PIR; PH1119; PH1119.

R PIR; PH1119; PH1119.

R PIR; PH1125; PH1126.

R PIR; PH1126; PH1126.
                                                                                                                     1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sclurognathi,
   Score 478.5; DB 2; Length 458;
                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                 .2e-42;
                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSMUSG0000021155; Mus musculus.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SWART; SM00406; IGV; 1.
                 Pred. No. 1
                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
WH186.2-D-J-C mu protein (Fragment).
76.9%;
                                                                                                                                                                                                                                                                                       Q924R8_MOUSE PRELIMINARY;
                               93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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PIR, PH1152, PH1152.
PIR, PH1153, PH1153.
HSSP, P01751, 1A6W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                 Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q924R8; 1-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=3135311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
                                                                                                                                                                                 118 S 118
                                                                                                                                                                                                              136 S 136
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   Query Match
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MEDINE-22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
MALAUSER R.D., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,
MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
MALSCHUL S.F., Jordan H., Moore T., Max S.I., Wang J., Haishe F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Malkesley R.W., Touchman J.W., Gereen E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.",
                                ö
                                                             1 QVQLQQPGAEVVKPGASVKMSCKASGYŢFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                            QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
                                                                                                                     61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project;
Submitted (MRX-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity)
-!- SMBCELLULAR LOCATION: Secreted (By similarity).
EMBL; BCO91272; AAH91272.1; -; mRNA.
SMR; QSBJZ2; 21-454.
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77.7%; Score 484; DB 2; Length 143; 76.3%; Pred. No. 7.4e-44; ive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00110; Ig-like.
InterPro; IPR003199; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_v.
Pfam; PF07654; Cl-set; 3.
SWART; SW00409; IG; 3.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
Immunoglobulin domain; Repeat.
SEQUENCE 458 AA; 50161 MW; AOAGIDCDD2CA433E CRC64;
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                              458 AA
                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                       10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
10-CG57586 protein.
Name=LOC367586;
                             90; Conservative
                                                                                                                                                                                                                         QSBJZ2_RAT PRELIMINARY;
QSBJZ2;
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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                 Similarity
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 Query Match
                 Best Local
Matches 9
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Q5BJZ2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDDNSGGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                 Gaps
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01-007-2003 (TrEMBLrel. 25, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                      DB 2; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
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                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                           16216 MW; 92460F1FDF1B7538 CRC64;
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                                                                                                                                                                                                                            y Match 76.6%; Score 477.5; DB 2; Local Similarity 74.4%; Pred. No. 3.8e-43; hes 90; Conservative 12; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AA.
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EMBL; U78801; AAD00293.1; -; mRNA.
HSSP; P01751; 1NQB.

SMR; O921C4; 1-118.
Ensembl; ENSWUSG0000021155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR007596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
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PROSITE; PS50835; IG_LIKE; 1.

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Q9Z1C4;
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NUCLEOTIDE SEQUENCE.
                                                                                                                                           146 AA;
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NON TER
SEQUENCE
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                                                                                                                                 SEQUENCE
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613 AA

PRT;

QBVCX7\_MOUSE PRELIMINARY;

RESULT 8 Q8VCX7 MOUSE ID Q8VCX7 MC

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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunzratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Rediguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Sikder S. K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
Morrison S.L., Kabat E.A.;
Morrison S.L., Kabat E.A.;
"Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1---6)dextrans.";
J. Immunol. 142:888-893(1989).
EMBL, BC018315; AAH18315.1; -; mRNA.
PIR; C30562, C30562.
HSSP; P01751; 1A6W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR0035965; Ig_V.
Pfam; PF07654; C1-set; 4.
                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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NUCLEOTIDE SEQUENCE.
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                                                                                                                  Igh-6 protein.
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1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
                                                           NOKFOCKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                           NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAKRSNYGAFDVWGTGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C., "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of C57BL/6 mice by BALB/C anti-idiotypes stimulates similar strain-specific V genes as the original antigen.";
J. Immunol. 141:779-784 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=3211160;
Kaartinen M., Rocca-Serra J., Makela O.;
"Combinatorial association of V genes: one VH gene codes for three
non-cross-reactive monoclonal antibodies each specific for a different
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/\bar{6};
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
VH186.2-J-J-C mu protein (Fragment).
                                                                                                                                                                                                                                         145 AA
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Mol. Immunol. 25:859-865(1988).
EMBL; AB067787; BAB63272.1; -; mRNA.
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PIR; JL0078; JL0078
PIR; PH1105; PH105.
PIR; PH1106; PH106.
PIR; PH1114; PH1114.
PIR; PH1114; PH1118.
PIR; PH1129; PH1126.
PIR; PH125; PH1126.
PIR; PH125; PH1126.
PIR; PH1129; PH1126.
PIR; PH1129; PH1129.
PIR; PH1139; PH1131.
PIR; PH1131; PH1131.
PIR; PH1131; PH1131.
PIR; PH1131; PH1131.
PIR; PH1139; PH1131.
PIR; PH1144; PH1144.
PIR; PH1149; PH1141.
PIR; PH1149; PH1141.
PIR; PH1151; PH1151.
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Q924R3;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kozono Y., Kozono H., Azuma T., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB067782; BAB63267.1; -; mRNA.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG-MHC; UNKNOWN_3.
Immunoglobulin domain.
SEQUENCE 613 AA; 67855 MW; 41A93384DD4C22862 CRC64;
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Last annotation update)
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                         88; Conservative
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Q924R7;
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PH1153; PH1153
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PH1118;
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PH1128;
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PH1149;
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RC TISSUE-Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

RX MEDINE-2388257; bubMed-12477932; DOI-10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RH Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soarse M.B., Bonaldo M.F., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Wakin T.B., Tooshiyuki S., Carninci P., Gunarane P.H.,

RA Brownstein M.J., Wakin T.B., Tooshiyuki S., Carninci P., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hitlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hitlan M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

ROMINION AND RATING M.I., Schalska U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski, M.I., Skalska U., Smallus D.E.,

RA Benerzation and initial analysis of more than 15,000 full-length human merch and monse chus
                                                                                                                                                                                     61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV--RLRYFDVWGQGTTVTVSS 118
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                             Gaps
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018280; AAH18280.1; -; mRNA.
RHSSP; PO1865; LRSB.
RMR; Q6PJB2; 20-461.
RMG; MG1943; Igh-1a.
RGJ; MG19643; Igh-1a.
RGJ; MG19829; Igh-1a.
R InterPro; IPR007110; Igh-1ke.
R InterPro; IPR007110; Igh-1ke.
R InterPro; IPR007110; Igh-1ke.
R InterPro; IPR007100; Igh-1ke.
R InterPro; IPR003006; Igh-1ke.
                                                            Length 145;
                                                            Query Match 75.6%; Score 471; DB 2; Length 14 Best Local Similarity 75.0%; Pred. No. 1.9e-42; Matches 90; Conservative 12; Mismatches 16; Indels
   1 1
145 145
145 AA, 15996 MW, 35B1A36E4280BA81 CRC64;
                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                               QEPJB2 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Czech II;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLKQSGAELVKPGASVKLSCKASGYTFNSYIMHWYKQRPGQGLEWIGYFSPYNDDTKC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFOGKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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-I- MISCELLANEOUS: This protein binds dextran.
-I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-80078170; PubMed-6765983;
Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran and DNA
tearrangements in heavy chain V-region gene segments.";
                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                        Length 465;
                                                                                                                                                                                                                                                                                                                                                             15; Indels
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS500835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein:
SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 116 IG-like.
22 96 By similarity.
117 117
117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; I.
BroSITE; PS50815; IG_LIKE; I.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                  Query Match 75.6%; Score 471; DB 2; Best Local Similarity 75.4%; Pred. No. 7.6e-42; Matches 89; Conservative 12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-VMY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region J558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
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By similarity.
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HSSP; P01751; 1NQB.
SMR; P01757; 1-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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Matches 90; Conserv
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P01757;
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Mnt1 model.

RE EXPINE=ZECH II;

RE EXPINE=ZECH II;

REDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RISURS=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RISURS=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RISURS=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RISURSER R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Ratusher R.D., Collins F.S., Beat N.K., Ramer A.H., Rubin G.M., Hong L.,

RALBOKHIS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blackleton M., Soares M.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Potens G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ritchards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYMMHWVKQRPQQGLEWIGNINPSNGGTNY 60
                                                                                                                                            61 NEKFKSKATLIVDKSSSTAYMQLSSLISEDSAVYYCARR-GWEAMDYWGQGTSVIVSS 117
                                                                                                                     NOKFOGKATLIADKSSTTAYMOLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                    QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIXPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sclurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 470.5; DB 2; Length 470; Pred. No. 8.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Strausberg R.;
L Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BCO55910; AAB55910.1; -; mRNA.
R HSSP; PO1865; 1KB5.
R GO: 00003823; F:antigen binding; IEA.
R InterPro; IPR003597; Ig_cl.
R InterPro; IPR003596; Ig_v.
R InterPro; IPR003596; Ig_v.
R InterPro; IPR003596; Ig_v.
R Fam; PP07654; Cl-set; 3.
R Pfam; PP07654; Cl-set; 3.
R RAMAT; SM00446; IGv; ILXR; 4.
DR ROSITE; PS00290; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KWAPCHCical protein; Immunoglobulin domain.
KW Hypothetical protein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein Al324046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                       Q7TMK1 MOUSE PRELIMINARY;
Q7TMK1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=AI324046;
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1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                            SULLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                              61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
                                                                                                                     Schiff C.;

Lumunization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCLEOTIDE SEQUENCE.

MUCLEOTIDE SEQUENCE.

MEDDLINE=22381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;

MEDLINE=22381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;

The sequence of the sequence of the sequence of clonally sequence of minimum and ing anti-DNA antibodies are the products of clonally sequence of sequence of the seq
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=3135311;
Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
"Allogeneic manipulation of the GAT idiotypic cascade. Immunizat:
G57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
J. Immunol. 141:779-784(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S., "Two murine natural polyreactive autoantibodies are encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.5%; Score 470.5; DB 2; Length 142; Best Local Similarity 75.4%; Pred. No. 2.1e-42; Matches 89; Conservative 11; Mismatches 17; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15622 MW; 24A265CE4EA4318B CRC64;
                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
V23-D-JC mu protein (Fragment).
Name=AB069917; Synonyms=V23-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonmutated germ-line genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989)
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                                                                                                                                                                                                                                                                  Q924Q1_MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00529; AAA38170.1; -; mRNA.

R PDB; 1A60; X-ray; H=20-139.

R PDB; 1A6V; X-ray; H=20-139.

R PDB; 1A6V; X-ray; H=20-139.

R PDB; 1A6V; X-ray; H=20-139.

R PDB; 1NGP; X-ray; H=20-139.

R PDB; 1NGQ; X-ray; H=20-139.

R PDB; 1NQC; X-ray; A/C=20-139.

R PDB; 1NQC; X-ray; A/C=20-139.

R InterPro; 1PR007310; Ig-1ike.

R InterPro; 1PR003596; Ig-v.

R SMART; SM00466; IG-v.

R PROSITE; PSS0835; IG LIKE; 1.

R ADD-etructure; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                     9
                                              79
                                     20 EVQLQQSGPBLVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                   "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                         QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
   3; Gaps
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1; Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region B1-8/186-2.
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Framework-2.
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 16; Indels
                                                                                                                                                                                                 HY07_MOUSE STANDARD; PRT; 139 AA. P01751; P01752; 139 AA. P01751; P01752; 21-UUL-1986 (Rel. 01, Last sequence update) 10-MAY-2005 (Rel. 01, Last annotation update) 10-MAY-2015 (Rel. 47, Last annotation update) Mus musculus (Mouse).
  14; Mismatches
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By similarity.
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  88; Conservative
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Best Local Similarity 74.2*
Matches 89; Conservative
139 AA;
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Search completed: May 9, 2006, 01:32:35 Job time : 109.039 secs

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Sequence 48,
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                GenCore version 5.1.8
(c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-238-741-4

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US-08-475-813-6

US-08-579-378A-7

PCT-US93-11612-7

PCT-US93-11612-7

PCT-US93-11612-7

US-09-724-138-44

US-09-724-138-44

US-09-724-138-44

US-08-403-853-18

US-08-860-174A-12

US-09-423-439-38

US-09-423-439-36

US-08-881-037-60

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US-08-881-037-60
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
Therapeutic Application of Chimeric and Radiolabeled Antibodies to Human B Lymphocyte Restricted Differentiation Antigen for the Treatment of B-Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFOCKATLTADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: W6/8476,275
FILING DATE: US/08/476,275
FLING DATE: US/08/476,275
FLING DATE: US/08/476,275
FLING APPLICATION TAR:
APPLICATION NUMBER: US/08/149,099
FLING APPLICATION NUMBER: US/08/149,099
FLING APPLICATION NUMBER: US/07/978,891
FLING APPLICATION NUMBER: US/07/978,891
FLING APPLICATION NUMBER: US/07/978,891
FLING DATE: 13-NOV-1992
ATTOMENY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 516.5; DB 1;
Pred. No. 6.5e-41;
9; Mismatches 11;
  TITLE OF INVENTION: Therapeutic Application TITLE OF INVENTION: Radiolabeled Antibodies TITLE OF INVENTION: Differentiation Antigen NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08475813
Patent No. 6682734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.9%;
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 140 amino acids
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amino acid
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Best Local Similarity 81.0
Matches 98; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                        CITY: Alexandria
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Leonard, John E.
Newman, Roland A.
Reff, Mitchell E.
Rastetter, William H.
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1 QVQLQQPGABVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
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Sequence 7, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
CITY: California
COUTRY: USA
                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION INMER: US/08/766,350B
FILING DATE: 13-Dec-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERING M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20003.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAR: (415) 813-5600
TELEFAR: (415) 813-5600
TELEFAR: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

80.6%; Score 502; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 1.2e-39;
Matches 93; Conservative 11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPERATION
COMPUTER: PROPERATION
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-766-350B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QVQLQQPGAELVKAGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
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TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
11D10 AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                          STREET: byy FILINGE SC.

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/08/475,813
FILING DATE: 07-JUN-1995
CLASSIPPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 13-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN I.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET UNBER: 35,030
REFERENCE/DOCKET UNBER: 35,030
REFERENCE/JOCKET UNBER: 35,030
REJEFAK: 703-835-6620
TELEFRAM: 703-835-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 516.5; DB 2;
Pred. No. 6.5e-41;
9; Mismatches 11;
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/08766350B
Patent No. 6949244
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.9%;
Best Local Similarity 81.0%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 140 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-475-813-6
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US-08-766-350B-48
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STRANDEDNESS: single
TOPOLOGY: linear
                                      TOPOLOGY: linear MOLECULE TYPE: protein
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    amino acid
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Best Local Similarity
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PCT-US93-11612-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                        Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREST: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 194105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: PCT/US93/11612
                                                                                                                                                                                                                                                                                                                                                                      80.5%; Score 501.5; DB 2; 77.7%; Pred. No. 1.4e-39;
              APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFIECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application PC/TUS9311612 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.7%;
****hes 94; Conservative
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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61 NQKPQGKATLIADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                               61 NEKFKGKATLITSDKSSSTAYMELSSLTSEDSAVYYCAREEYGNYVRYFDVWGAGTTVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                         Gaps
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     Length 121;
                                                         12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Knoulle and Cond
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11612
Query Match 80.5%; Score 501.5; DB 4; Best Local Similarity 77.7%; Pred. No. 1.4e-39; Matches 94; Conservative 12; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/ABENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 140 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Conservative
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61 NOKFOGKATLITADKSSTTAYMOLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTTVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 498; DB 2; Length 140;
Pred. No. 3.4e-39;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRAING SYSTEM: US/08/403,853

FILING DATE: 30-MAY-1995

CLASSIFICATION NUMBER: WO PCT/AU93/00491

PILING DATE: 24-SEP-1993

PROFINGATION NUMBER: WO PT/AU93/00491

PILING DATE: 25-SEP-1992

PILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOler
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 08/471984
PRIOR FILING DATE: 1995-06-06
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1988-05-13
PRIOR APPLICATION NUMBER: US 07/195961
PRIOR PILING DATE: 1987-01-08
PRIOR PILING DATE: 1987-01-08
PRIOR FILING DATE: 1987-01-08
PRIOR FILING DATE: 1987-01-08
PRIOR FILING DATE: 1986-10-27
PRIOR FILING DATE: 1986-10-27
PRIOR FILING DATE: 1986-10-27
SOFTWARE: PATCHIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/08403853 Patent No. 5844094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRVING, Robert A. ATWELL, John L. MALBY, Robyn L. POWER, Barbara E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.9%;
Best Local Similarity 78.5%;
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Mus musculus
US-09-630-198-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 S 140
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 140
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robinson, Randy
APPLICANT: Liu, Alvin
APPLICANT: Liu, Alvin
APPLICANT: Ledbetter, Jeffrey
TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/09630198

Patent No. 6893625

GENERAL INFORMATION:
APPLICANT: Robinson, Randy
APPLICANT: Liu, Alvin
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Ledbetter, Jeffrey
TILE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti
FILE REFERENCE: PPL-001CN
CURRENT APPLICATION NUMBER: US/09/630,198
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 09/021934
                                     61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTTVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 NQKPKGKATLITVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.9%; Score 498; DB 2; Length 140; 78.5%; Pred. No. 3.4e-39; ive 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILE KEFEKENCE: PFU-001CLE
CURRENT APPLICATION NUMBER: US/09/724,138
CURRENT PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 1998-02-12
PRIOR PELING DATE: 1998-02-12
PRIOR PELING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 04/71984
PRIOR FILING DATE: 1995-06-06
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PILING DATE: 1991-03-05
PRIOR PELING DATE: 1988-05-13
PRIOR PELING DATE: 1988-05-13
PRIOR PILING DATE: 1988-01-03
PRIOR PILING DATE: 1988-05-13
                                                                                                                                                                                                                                                                                                       Sequence 44, Application US/09724138
Patent No. 6652852
GENERAL INFORMATION:
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Best Local Similarity 78.5°
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-09-724-138-44
                                                                                                               118 S 118
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SEQ ID NO 44
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REFERENCE/DOCKET NUMBER: 11823-002220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCARE-VRLRY---FDVWGQGTTVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 QVQLQQSGAELVKPGASVRMSCKASGYTFTNYNMYWXQSPGQGLEWIGIFYPGNGDTSY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.5%; Score 495; DB 1; Length 273; Best Local Similarity 78.5%; Pred. No. 1.4e-38; Matches 95; Conservative 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRIE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSITCATION ADATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-ANG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-ANG-1995
FILING DATE: 19-SEP-1995
ATTONNEY/AGENT INFORMATION:
ANDER TICKNEY/AGENT INFORMATION:
ANDER TI
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REDESTRATION NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08579378A Patent No. 6210671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-853-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 S 117
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US-08-579-378A-4
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61 NOKFOGKATLITADKSSTTAYMQLSSLTSEDSAVYYCAREV---RLRYFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 NEKFKGKATLITSDKSSSTAYMELSSLTSEDSAVYYCAREEYGNYVRVFDVWGAGTTVTVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYIYPYNDGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113, Application US/09419788

Sequence 113, Application US/09419788

Batent No. 6825325

GENERAL INFORMATION:

APPLICANT: FISCHER, Rainer

APPLICANT: SCHILLBERG, Stefan

APPLICANT: SCHILLBERG, Stefan

APPLICANT: SPISCHER, Michael

APPLICANT: SPISCHEL, Holger

APPLICANT: SPISCHEL, Holger

APPLICANT: EMANS, Neil

TITLE OF INVENTION: Medicular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Resistance

TITLE OF INVENTION: Resistance

TITLE OF INVENTION: Weststeance

FILE REFERENCE: 0147-0189P

CURRENT APPLICATION NUMBER: US/09/419,788

CURRENT FILING DATE: 1999-10-18

EARLIER FILING DATE: 1998-10-16

SARLIER FILING DATE: 1998-10-16

NUMBER OF SEC ID NOS: 163

SOFTWARE: PATENTION NUMBER: 66/BOM/1998 INDIA

SEQ ID NO 113

SERQ ID NO 113

LENGTH: 05-7
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
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                                                                                                                                                                                                                                                                                                                 Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.0%; Score 492; DB 2; Length 257; Best Local Similarity 78.8%; Pred. No. 2.4e-38; Matches 93; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                              79.2%; Score 493.5; DB 2
76.9%; Pred. No. 9.1e-39;
cive 12; Mismatches 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                             : 140 amino acids
amino acid
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.9*
Matches 93; Conservative
                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-579-378A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 QVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYIYPYNDGTKY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
63 NOKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARP-----DVWGAGTLLTVSA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEKFRGKATLTSDKSSSTAYMELSSLTSEDSAVYYCSRR-----FDYWGQGTTVTVSS 135
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Patent No. 59898130

GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLESURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                            APPLICANT: DANIS, Paul James
APPLICANT: DANIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Brik
APPLICANT: VERNOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS DOS TEXT
SOFTWARE: MS WORD, WINNOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: JUME 16, 1997
PRION APPLICATION DATA:
APPLICATION NUMBER: EP 9530733.7
FILING DATE: OCCODET 16, 1995
APPLICATION NUMBER: PCT/ER/96/03605
FILING DATE: AUGUST 14, 1996
INPORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.7%; Score 490.5; DB 1
78.0%; Pred. No. 1.7e-38;
trive 10; Mismatches 11
                                                                                                                       Sequence 4, Application US/08860174A; Patent No. 5989830; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 78.0
Matches 92; Conservative
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                                                                                                       US-08-860-174A-4
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162 QVQLQQSGPELVKPGASVKMSCKASGYTFISYVMHWVKQKPGQGLEWIGYIYPYNDGTKY 221
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                                                                                                                                                                               DOS Text
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparation
OPERATING SYSTEM: PC-DOS/MS-DOS DOS TY
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATE: PS307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: EP 9530733.7
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 9, 2006, 01:35:40 Job time: 27.5628 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                       ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-860-174A-12
                                                  COUNTRY:
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Wed May 10 09:27:26 2006

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
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Sequence 9, Application US/10700632
| Publication No. US20050118183A1 |
| Sequence 9, Application No. US20050118183A1 |
| GENERAL INFORMATION: APPLICANT: ImmunoGen, Inc. |
| TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID TITLE OF INVENTION: LEUKEMIA USING THE SAME FILE REFERENCE: A8427 |
| TITLE OF INVENTION: LEUKEMIA USING THE SAME FILE REFERENCE: A8427 |
| CURRENT APPLICATION NUMBER: US 60/424,332 |
| PRIOR PELLING DATE: 2003-11-07 |
| NUMBER OF SEQ ID NOS: 94 |
| SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 9 |
| LENGTH: 118 |
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TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REFERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT FILING DATE: 2003-11-05
PRIOR APPLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
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iive 0; Mismatches 0;
US-10-822-231-5
US-10-723-003-40
US-11-019-180-4
US-11-004-639-44
US-11-004-639-44
US-11-004-639-46
US-11-004-639-48
US-11-004-639-68
US-10-917-599-1
US-10-917-599-1
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ORGANISM: Artificial Sequence
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APPLICANT: Goshorn, Stephen C.
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                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTI-CC33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID TITLE OF INVENTION: ALLICASIA ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID TITLE OF INVENTION: LEUKEMIA USING THE SAME FILE REFERENCE: A8427

CURRENT APPLICATION NUMBER: US/10/700,632

CURRENT FILING DATE: 2003-11-05

PRIOR APPLICATION NUMBER: US 60/424,332

PRIOR PILING DATE: 2002-11-07

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PATENTIAN OF SEQ ID NOS: 94

SOFTWARE: ALENETH VERSION 3.2

LENGTH: 117
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                                                                                                                                                                                                                                            1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                                                                                                                                                                                                                          1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIXPGNDDISY 60
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                                                                                                                                                                                                                                                                                                                                      NOKFOCKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVSS 118
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Publication No. US20030219433A1
Publication No. US20030219433A1
APPLICANT: HANSEN, HANS
APPLICANT: QU, ZHENGXING
APPLICANT: QU, ZHENGXING
TITLE OF INVENTION: MATH-CO20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NOKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLRYFDVWGQGTTVTVS 117
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0
                                                                                                                                                            Length 118;
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                                                                                                                                                       Score 613; DB 5; Length 11
Pred. No. 8.4e-46;
1; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR PELING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PALENTIN Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-10-632-73
Sequence 73, Application US/10700632
Publication No. US20050118183A1
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.2 SEQ ID NO 7
                                                                                                                                                       Query Match
Best Local Similarity 98.3%;
Matches 116; Conservative
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Matches 115; Conservative
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; ORGANISM: Mus musculus
US-10-700-632-73
                                                                                  ; ORGANISM: Mus musculus
US-10-700-632-7
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US-10-366-709-39
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Sequence 35, Application US/10366709

Sequence 35, Application No. US2003021943341

GENERAL INFORMATION:
APPLICANT: HANSEN, HANS

APPLICANT: QU'ZHENDRING
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 18733/115

CURRENT APPLICATION NUMBER: US/10/366,709

CURRENT APPLICATION NUMBER: 60/356,132

PRIOR APPLICATION NUMBER: 60/416,232

PRIOR APPLICATION NUMBER: 60/416,232

PRIOR FILING DATE: 2002-10-14

PRIOR FILING DATE: 2002-10-14

SEQ ID NOS: 55

SOFTWARE: Patentin Ver: 2.1

SEQ ID NOS: 55
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US-10-366-709-35
                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy OTHER INFORMATION: chain cA20VH amino acid sequence
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                                                                                                                                                                                                                                                                Query Match 86.4%; Score 538.5; DB 4; Length 121; Best Local Similarity 84.3%; Pred. No. 2.6e-39; Matches 102; Conservative 7; Mismatches 9; Indels 3
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SEQ ID NO 39
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
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188 NQKFKGKATLTADKSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTV 246
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APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THEAPERPETTIC APPLICATION OF CHIMERIC AND RADIOLABELED TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL TITLE OF INVENTION: LYMPHOWA.
FILLE REPERENCE: 37003/0291808
CURRENT APPLICATION NUMBER: US/10/238,681
CURRENT FILING DATE: 2002-09-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain OTHER INFORMATION: antibody-genomic streptavidin fusion
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                                  61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR-
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Graves, Scott Stoil
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GEN
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goshorn, Stephen Charles APPLICANT: Graves, Scott Stoll
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                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10244821
Publication No. US20030143233A1
GENERAL INFORMATION:
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                                                                                                                                  117 SS 118
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Publication No. US20030103948A1

GENERAL INFORMATION:

APPLICANT: Goshorn, Stephen C.

APPLICANT: Goshorn, Stephen C.

APPLICANT: Schiltz, Joanne E.

APPLICANT: Schiltz, Joanne E.

APPLICANT: Sanderson, James A.

APPLICANT: Sanderson, James A.

APPLICANT: Sanderson, James A.

TITLE OF INVENTION: STREETANDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REPERENCE: 69022.547C2

CURRENT APPLICATION NUMBER: US/10/150,762
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Eanderson, James A.
APPLICANT: Reno, Jonh M.
APPLICANT: Reno, Jonh M.
APPLICANT: Reno, Jonh M.
TITLE OF INVENTION: STREEPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: BRITHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US,10/013,173
CURRENT PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 84.3%; Score 525.5; DB 4; Length 412; Best Local Similarity 83.6%; Pred. No. 1.2e-37; Matches 102; Conservative 7; Mismatches 8; Indels 5
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-013-173-6
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Gaps

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US-10-411.026-62

Sequence 65. Application US/10411026

Publication No US20040063911A1

GRENEAL INFORMATION:

APPLICANT: NPOSMETON:

APPLICANT: DeFrees, Shawn

APPLICANT: Bayer, Robert

APPLICANT: Bayer, ROBERTON:

ITILE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

ITILE OF INVENTION: WINDER: US/10/411,026

CURRENT APPLICATION NUMBER: US/03-89

FRICK APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PLING DATE: 2001-10-19

PRIOR PLING DATE: 2001-10-19

PRIOR PLING DATE: 2002-06-05

PRIOR PLING DATE: 2002-06-05

PRIOR PLING DATE: 2002-06-07

PRIOR PLING DATE: 2002-07-17

PRIOR PLING DATE: 2002-07-17

PRIOR PLING DATE: 2002-08-16

PRIOR PLING DATE: 2002-08-16
                                                                                                                                                                                                                                            80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVS 139
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                                                                                                                                                                                                    61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                               QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
                                                                                          20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
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US-10-410-962-62
Sequence 62, Application US/10410962
; Publication No. US20040077836A1
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US-10-411-026-62
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SEQ ID NO 62
LENGTH: 140
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF GALACTOSIDASE
TILLS OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF GOI-0-10
PRIOR PELLING DATE: 2001-0-10
PRIOR PELLING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PELLING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-26
PRIOR PELLING DATE: 2002-06-36
PRIOR PELLING
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81.8%; Pred. No. 5.1e-38;
ive 9; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 524.5; DB 4; Length 1 Pred. No. 5.1e-38; 9; Mismatches 10; Indels
PRIOR APPLICATION NUMBER: 08/921,060
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR PRILING DATE: 1993-11-03
PRIOR FILING DATE: 1993-11-03
PRIOR FILING DATE: 1992-11-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
LENGTH: 140
LENGTH: 140
TYPE: PRT
TYPE: PRT
CREAMING Murine sp.
US-10-238-681-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%;
Matches 99; Conservative
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Best Local Similarity 81.8
Matches 99; Conservative
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US-10-411-037-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Mitko SAUURADA
APPLICANT: Mitko SAUURADA
APPLICANT: Mitko SAUURADA
APPLICANT: Mitko SAUURADA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Mitsuo SATOH
TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
FILE REFERENCE: 249-289
CURRENT APPLICATION NUMBER: US/10/327,663
CURRENT APPLICATION NUMBER: US/2001-392753
PRIOR APPLICATION NUMBER: UP 2001-392753
PRIOR APPLICATION NUMBER: UP 2002-106948
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 63
SOFTWARE PATENTIN VOS: 63
SOFTWARE PATENTIN VOS: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQPGAELVKPGASVKASCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY
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81.8%; Pred. No. 5.1e-38;
tive 9; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%; Score 524.5; DB 4; Length 140;
81.8%; Pred. No. 5.1e-38;
ive 9; Mismatches 10; Indels 3
PRIOR APPLICATION NUMBER: US 60/381,232
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/306,594
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-18
PRIOR PLING DATE: 2002-08-28
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Publication No. US20040093621A1
GENERAL INFORMATION:
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Best Local Similarity 81.8
Matches 99; Conservative
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Matches 99; Conserva
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; Sequence No. US20040082026A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Defrees, Shawn
; APPLICANT: Defrees, Shawn
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Bowe, Caryn
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: ALPHA S.
FILLE REFERENCE: O40853-01-5055
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR APPLICATION NUMBER: US 60/324,692
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-19
                                                                                                                                                  APPLICANT: Bayer. Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Howe, Caryn
TITLE OF INVENTION: GLYCOCOUNTGATION OF G-CSF
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-66-25
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-15
PRIOR PILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
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81.8%; Pred. No. 5.1e-38;
ive 9; Mismatches 10; Indels 3
                            Neose Technologies, Inc.
DeFrees, Shawn
Zopf, David
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Best Local Similarity 81.8
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 S 118
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US-10-410-930-62

Sequence 62, Application US/10410930

Publication No.

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Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps
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; ORGANISM: Mus musculus
US-10-410-930-62
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Sequence 92, Appl
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Sequence 22, Appl
Sequence 24, Appl
Sequence 19, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/11107028
; Sequence 35, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QLAN
; TITLE ON UNIVERTION: Method for Augmenting B Cell Depletion
; TITLE ON UNIVERSION: Method for Augmenting B Cell Depletion
; FILE REPERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR PRILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 35
; LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.4%; Score 538.5; DB 11; Length Best Local Similarity 84.3%; Pred. No. 4.1e-36; Matches 102; Conservative 7; Mismatches 9; Indels
                                                                                         US-10-507-662-32

US-10-932-334-13

US-11-932-334-88

US-10-932-334-88

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US-10-932-334-89

US-10-932-334-82

US-10-932-334-22

US-10-932-334-72

US-10-932-334-72

US-11-297-317-4

US-11-297-317-4

US-11-226-325-198

US-11-226-325-21

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US-11-226-325-10
                                                        US-11-069-834-2
US-11-054-669-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-11-183-218-62
Sequence 62, Application US/11183218
Publication No. US20060088906A1
   ORGANISM: Artificial sequence
     $ 121
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388.792 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
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1 QVQLQQPGAEVVKPGASVKM......EVRLRYFDVWGQGTTVTVSS
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1: /SIDS5/ptodata/2/pubpaa/USO8_NEW_PUB.pepl:*
2: /SIDS5/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
9: /SIDS5/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
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                       GenCore version 5.1.8
(c) 1993 - 2006 Biocceleration Ltd.
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US-11-183-218-62
US-11-184-620-5
US-11-124-620-7
US-11-126-928-25
US-11-126-928-28
US-11-126-928-7
US-11-106-920-7
US-11-106-920-7
US-11-107-38-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-143-386-7
US-11-100-820-18
US-11-100-928-37
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US-11-107-028-37
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 200000000
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                                         APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Gho, Xi
APPLICANT: Bowe, Caryne
APPLICANT: Bowe, Caryne
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
TITLE OP INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
FILE REFERENCE: 040853-01-5083-US02
CURRENT PELING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 10/410,945
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-28
PRIOR PILING DATE: 2001-11-38
PRIOR PILING PILING DATE: 2001-11-38
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
ITILE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REPERENCE: 040853-01-5052-US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 62, Application US/11183205; Publication No. US20060030521A1
Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-11-183-218-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S 118
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| CURRENT APPLICATION NUMBER: 109/11/103, 205
| PRIOR PAPLICATION NUMBER: 109 11/103, 205
| PRIOR PAPLICATION NUMBER: 109 11/103, 205
| PRIOR PAPLICATION NUMBER: 109 11/103, 205
| PRIOR PAPLICATION NUMBER: 108 10/134, 233
| PRIOR PAPLICATION NUMBER: 108 10/134, 234
| PRIOR PAPLICATION NUMBER: 108 10/134, 234
| PRIOR PAPLICATION NUMBER: 108 10/134, 234
| PRIOR PAPLICATION NUMBER: 108 10/140, 243
| PRIOR PAPLICATION
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61 NQKFKGKATLIADKSSSTAYMQLSSLISEDSAVYCARSTYYGGDWYFNVWGAGTTVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY 60
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Publication No. US20060067930A1
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Marvin, Jonathan S.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Marvin, Doughan, Wolvpeptide Variants with Altered Effector Function
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P2158R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 524.5; DB 1:
Pred. No. 1.6e-34;
9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE KEFREKECK A-71386-9
CURRENT PELICATION NUMBER: US/11/124,620
CURRENT PILING DATE: 2005-05-05
FRIOR APPLICATION NUMBER: US 60/568,440
PRIOR FILING DATE: 2004-07-15
FRIOR FILING DATE: 2004-07-15
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-11-09
FRIOR FILING DATE: 2004-11-09
FRIOR FILING DATE: 2004-11-10
FRIOR FILING DATE: 2004-11-12
FRIOR FILING DATE: 2004-03-26
FRIOR FILING DATE: 2004-03-26
FRIOR FILING DATE: 2003-09-26
FRIOR FILING DATE: 2003-09-26
FRIOR FILING DATE: 2003-09-26
FRIOR FILING DATE: 2003-09-26
FRIOR FILING DATE: 2003-09-36
FRIOR FRIUNG DATE: 2003-09-36
FRIOR FRIUNG DATE: 2003-09-36
FRIOR FRIUNG DATE: 2003-09-37
FRIOR FRIUNG DATE: 2003-09-37
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Desjarlais, John R.
APPLICANT: Karki, Sher Bahadur
APPLICANT: Vafa, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
                                                                                                                                                                                                        ; Sequence 7, Application US/11124620 ; Publication No. US20060024298A1
                                                                                                                                                                                                                                          Publication No. US20060024298A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: Lazar, Gregory Alan APPLICANT: Dang, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
            118 S 118
                                                                  121 A 121
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LOCATION: (335)...(335)...(335)...
OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine
OTHER INFORMATION: or Glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (243)..(243)
OTHER INPORMATION: Kaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
OTHER INPORMATION: Clutamine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQKFQGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTTVTVS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (268)...(268)
OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (272]..(272)
OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (334)...(334)
OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
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LOCATION: (330)..(330)
OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (244)...(244)
OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (302)..(302)
OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.2%; Score 524.5; DB 11; Length
81.8%; Pred. No. 1.6e-34;
tive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (301)...(301)
OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: (276)...(276)
OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (278)...(278)
OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR PILING DATE: 2003-09-30
PRIOR FILING DATE: 2003-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.3
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic
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Best Local Similarity 81.8'
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial
                                                                                                                                                                                                                                             451
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US-11-254-182-28
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                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFOGKATLTADKSSTTAYMQLSSLTSEDSAVYYCAREVRLR---YPDVWGQGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLEWVGVIYPGNDDISY
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foon, Kenneth A. Chatterjee, Sunil K. Chatterjee, Sunil K. TITLE OF INVENTION: WIRINE MONOCIONAL ANTI-IDIOTYPE ANTIBODY 11110 AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                           <u>ښ</u>
                                                                                                                                                                                                                                                                            Query Match

84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DATH: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/126,798
FILING DATE: 10-May-2005
CLASSIFICATION NUMBER: US/08/836,455
FILING DATE: 09-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHORING:
REGISTRATION NUMBER: 40,130
REFERENCE/OCKET NUMBER: 30414-20003.22
TELECOMMUNICATION INPORMATION:
TELEPRAK: (650) 813-5600
THEERPAK: (650) 844-0792
                                                                                                                                                                                                             ; OTHER INFORMATION: sequence is synthesized US-11-208-422-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CURRENT APPLICATION NUMBER: US/11/208,422
             CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 25
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/11126798
Publication No. US20060018895A1
GENBERL INFORMATION:
APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: PALO ALTO STATE: CA
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121 A 121
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US-11-126-798-48
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61 NQKFKGKATLITVDKSSSTAYMQLSSLISEDSAVYFCARVVYSSNSYMYFDVWGTGTIVIV 120
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                                                                                                                                                                                                          1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYYIHWIKQTPGQGLBWVGVIYPGNDDISY
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                                                                                                                                                       Gaps
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                                                                                              Query Match 80.6%; Score 502; DB 11; Length 118; Best Local Similarity 78.8%; Pred. No. 3e-33; Matches 93; Conservative 11; Mismatches 14; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: GREWAL, IQBAL S.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION UNMBER: US/11/120,338
CURRENT APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ANDYA, JAMES
APPLICANT: GWEE, SHIANG C.
APPLICANT: LIU, JUN
APPLICANT: LIU, JUN
APPLICANT: SHEM, YE
TITLE OF INVENTION: ANTIBODY FORMULATIONS
FILE REFERENCE: P2104R1
CURRENT APPLICATION NUMBER: US 60/620,413
PRIOR APPLICATION NUMBER: US 60/620,413
PRIOR FILING DATE: 2004-10-20
PRIOR FILING DATE: 2004-10-20
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 28
LENGTH: 122
                  SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-126-798-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 28, Application US/11254182; Publication No. US20060088523A1; GENERAL INFORMATION:
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; Publication No. US20050271658A1
; GENERAL INFORMATION:
TOPOLOGY: linear
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US-11-254-182-28
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Best Local Similarity
Matches 96; Conserv
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61 NQKFKGKATLIYUDKSSSTAYMQLSSLISEDSAVYFCARVVYYSNSYWYFDVWGTGTITVIV 120
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Publication No. US2006002430041

PITLE REPERMER: P1990R3C1P1

CURRENT APPLICATION: Immunoglobulin Variants and Uses Thereof

PIER REPERMER: P1990R3C1P1

CURRENT PILING DATE: 2005-07-26

PRIOR PILING DATE: 2003-12-16

PRIOR PILING DATE: 2003-12-06

PRIOR APPLICATION NUMBER: US 60/526,163

PRIOR APPLICATION NUMBER: US 60/526,163

PRIOR PILING DATE: 2003-12-06

PRIOR PILING DATE: 2003-12-06
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                                                                                                                                                                                    80.6%; Score 502; DB 11; 78.7%; Pred. No. 3.1e-33; iive 8; Mismatches 14;
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Pred. No. 3.1e-33;
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Publication No. US20060034835A1
GENERAL INFORMATION:
APPLICANT: Adams BT AL.
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  PRIOR FILING DATE: 2004-10-11
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Best Local Similarity 78.7
Matches 96; Conservative
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                        NUMBER OF SEQ ID NOS: 24
SEQ ID NO 7
                                                                                                        , ORGANISM: Mus musculus US-11-143-077-7
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                                                                    LENGTH: 122
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                                                                                          Length 122;
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                                                                                                                                        Indels
                                                                                                                                             14;
                                                                                            DB 11;
                                                                                          Query Match

80.6%; Score 502; DB 11.
Best Local Similarity 78.7%; Pred. No. 3.1e-33.
Matches 96; Conservative 8; Mismatches 14
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Publication No. US20060024295A1

GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
TITLE OF INVENTION: METHOD FOR TREATING LUPUS
FILE REFERENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077

CURRENT FILING DATE: 2005-06-02

PRIOR APPLICATION NUMBER: US 60/577,235

PRIOR APPLICATION NUMBER: US 60/577,235

PRIOR APPLICATION NUMBER: US 60/577,997
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PUBLICALION NO. US20060002930A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G
APPLICANT: SEWELL, KATHRYN L.
TITLE OF INVENTION: Treatment of Disorders
FILLE REFERENCE: P2102R1
CURRENT APPLICATION NUMBER: US/11/106,820
CURRENT PILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,227
PRIOR APPLICATION NUMBER: US 60/563,227
PRIOR PELING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-22
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Matches 96; Conservative
    ) Tirb: FAA.
) ORGANISM: Mus musculus
US-11-120-338-7
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TYPE: PRT
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; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NOS: 38
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Bublication No. US20060051345A1;
GENERAL INPORMATION:
APPLICANT: FROHNA, PAULA;
ITILE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS;
FILE REPRENCE: P2134R1
CURRENT FILING DATE: 2005-06-02;
PRIOR APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02;
PRIOR APPLICATION NUMBER: US 60/576,993;
PRIOR PILING DATE: 2004-06-04;
NUMBER OF SEQ ID NOS: 25
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US-11-187-364-7
; Sequence 7, Application US/11187364
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Matches 96; Conservative
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ORGANISM: Mus musculus
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; ORGANISM: Mus musculus
US-11-147-780-7
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US-11-143-386-7
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      GENERAL INFORMATION:
APPLICANT: Hitraya, Elena
TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
FILE REFERENCE: P2149R1
CURRENT APPLICATION NUMBER: US/11/187,364
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/590,302
PRIOR PELING DATE: 2004-07-22
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 7
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Publication No. US20060062787A1
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US-11-187-364-7
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Best Local Similarity
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ado32094 Humanised Ado32092 Mouse ant Ado32146 Mouse ant Aea38741 Murine an Aea38768 Humanized Aar54933 MAD 022 V Adx37184 Murine SM Aea88701 Mouse ant Adv99246 Mouse SM5 Adv98529 Novel chi Adv99533 Novel chi Adv99533 Novel chi Adv98533 Novel chi Adv98533 Novel chi Adv98553 Novel chi Adv9805240 Attibody Aae22266 S. aureus Adv980226 Antibody Aae222670 S. aureus Adv980228 Antibody Aae20222 Antibody Aae20222 Antibody Aae30222 Antibody Aae30222 Antibody Aae30222 Antibody	
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anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised; Humanised mouse anti-CD33 antibody My9-6 light chain SEQ ID NO:10. AD032094 standard; protein; 113 AA Lutz RJ; 05-NOV-2003; 2003WO-US032737. 07-NOV-2002; 2002US-0424332P. (first entry) Hoffee MG, Tavares D, (IMMU-) IMMUNOGEN INC. WPI; 2004-411619/38. My9-6; light chain. WO2004043344-A2. Homo sapiens. Synthetic. 12-AUG-2004 Mus musculus 27-MAY-2004. AD032094; AD032094 

New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute or chronic myeloid leukemia.

Claim 14; SEQ ID NO 10; 124pp; English.

The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or

N-PSDB; ADO32139.

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composition comprising the immunoconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the defined antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above of defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its optiope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment to polymucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment of a recombinant vector comprising the polymucleotide, (11) a host cell transformed with the recombinant vector; (12) producing an antibody or a recombinant vector comprising the ability to bind CD33; and (13) cobtaining CD33 from a biological material. The antibody or its epitope-binding fragment, (10) cobtaining CD33 from a biological material captore-binding fragment, or immunoconjugate, composition can be used for treating a subject having a disease where CD33 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia, and for in vivo imaging or as affinity purification agents. The present composition which is used in an example from the present composition which is used in an example from the present
epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
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Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8. anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6; ADO32092 standard; protein; 113 AA. 05-NOV-2003; 2003WO-US032737 (first entry) WO2004043344-A2. Mus musculus. 12-AUG-2004 light chain. 27-MAY-2004 AD032092; RESULT 2 

Immunoconjugate comprising the antibody of the aptroperation compression of the antibody or composition comprising the antibody or epitope-binding fragment and a drug or producy; (3) a pharmaceutical composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polymucleotide encoding the antibody or its epitope-binding fragment; (10) a recombinant vector comprising the polymucleotide; (11) a host cell transformed with the recombinant vector; (12) producing a light or heavy chain of the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polymucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) cobtaining CD33 from a biological material. The anti-CD33 antibody has cytostatic activity. The antibody or its epitope-binding fragment, or immunoconjugate, composition can be used for treating a subject having a disease where CD3 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. It can also be used for timbiting the growth of cells expressing CD3, and for in vivo imaging or as affinity purification agents. The present invention.

Sequence represents the mouse anti-CD33 antibody My9-6 light chain or sequence represents the mouse anti-CD33 antibody My9-6 light chain. New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment 92.7%; Score 543; DB 8; Length 113; 93.8%; Pred. No. 7.4e-35; rive 3; Mismatches 4; Indels Claim 8; SEQ ID NO 8; 124pp; English. or chronic myeloid leukemia. Query Match Best Local Similarity Sequence 113 AA; 

61 61 2 IVLIQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE Gaps 62 SGVPDRFTGSGSGTDFTLTISSVQSEDLAIYYCHQYLSSRTFGGGTKLEIKR 113 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113 ö Matches 105; Conservative 62 ठ 셤 ઠ 셤

anti-CD33 antibody; epitope-binding fragment; complementarity-determining region; CDR; immunoconjugate; cytostatic; antibody; myelodysplastic syndrome; acute myeloid leukaemia; chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain. Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62 12-AUG-2004 (first entry) 

ADO32146 standard; protein; 114 AA

RESULT 3 AD032146 AD032146;

Mus musculus

Lutz RJ;

Tavares D,

Hoffee MG,

WPI; 2004-411619/38

07-NOV-2002; 2002US-0424332P

(IMMO-) IMMONOGEN INC

(first entry)

11-AUG-2005

AEA38741;

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The present invention describes an isolated anti-CD33 antibody or its comptope-binding fragment comprising: (a) at least one complementarity—determining region (CDR), or (b) at least heavy chain variable region comprising 13 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD3. Also described: (1) an immunocoligate comprising the antibody or its epitope-binding fragment in dargo or prodrug; (2) a composition comprising the antibody or its epitope-binding fragment composition comprising the immunocoligate, composition or the antibody or attained or prodrug; (3) a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody or the antibody or attained fragment is labelled; (5) inhibiting the agent; (4) a diagnostic reagent comprising the cell with the above defined antibody or its epitope-binding fragment is labelled; (5) inhibiting the contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment, immunoconjugate, or contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment (7) an improved antibody or its epitope-binding fragment (7) an improved antibody or heavy chain of the antibody or its epitope-binding fragment (7) are combinant vector comprising the polymucleotide encoding a light or heavy chain of the antibody or its epitope-binding fragment are exampled above; (9) an isolated polymucleotide encoding a light or heavy chain of the antibody or its epitope-binding fragment (7) are a recombinant vector; (12) producing an antibody or its epitope-binding fragment are polymucleotide, (11) a host cell coptaining CD33 from a biological material. The anti-CD33 antibody has cycostatic activity. The antibody or its epitope-binding a subject behaving a composition can be used for traating a subject behaving a composition can be used for the prosent or involved in an ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute
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The present invention relates to the screening of candidate molecules [anti-transforming growth factor (TGF)-beta antibodies] for the treatment core (anti-transforming growth factor (TGF)-beta antibodies] for the treatment core (at the invention involves administering several test screening method of the invention involves administering several test substances to a non-human syngeneic immunocompetent animal model bearing at least one soft tissue or bone metastasis optionally in presence of a primary tumor, determining the effects of these test substances on the soft tissue or bone metastasis and growth of the primary tumor and identifying a test substance inhibiting soft tissue growth or bone metastasis without adverse effect on the status of the primary tumor. The invention is useful in the diagnosis and treatment of breast cancer, colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer, liver and lung metastases, bone destruction and bone colorectal cancer. The prophylaxis or treatment of soft tissue and/or bone metastases which may additionally be effective in treating the primary tumor. The present sequence is murine anti-TGF-beta antibody cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening compounds useful for treating tumor metastasis involves administering a test compound to non-human animal model bearing soft tissue/bone metastasis and identifying compound that inhibits soft tissue
                                                                                                                   Monoclonal antibody, animal disease model, metastasis, cytostatic, neoplasm, bone metastases, breast tumor, colorectal tumor, bone disease, osteopathic, antibody therapy, radiation therapy, immunotherapy; cancer cell proliferation inhibitor;
                                                                                                                                                                                                          transforming growth factor-beta-antagonist; light chain variable region
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                                                                                  Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.
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31-MAR-2004; 2004US-0557951P.
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The present invention relates to the screening of candidate molecules [anti-transforming growth factor (TGF)-beta antibodies] for the treatment of funci metastasis and treatment methods using such molecules. The screening method of the invention involves administering several test substances to a non-human syngeneic immunocompetent animal model bearing at least one soft tissue or bone metastasis optionally in presence of a primary tumor, determining the effects of these test substances on the soft tissue or bone metastasis and growth of the primary tumor and identifying a test substance inhibiting soft tissue growth or bone metastasis without adverse effect on the status of the primary tumor. The invention is useful in the diagnosis and treatment of breast cancer, colorectal cancer, liver and lung metastases, bone destruction and bone lubstances useful for the present invention is useful to screen substances useful for the present extreatment of soft tissue and/or bone metastases which may additionally be effective in treating the growth factor-beta (anti-TGF-beta) antibody (also referred as humanized munine anti-transforming growth factor-beta (anti-TGF-beta) antibody (also referred as humanized munine anti-transforming monoclonal antibody 2G7) chimeric protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease; osteopathic; antibody therapy; radiation therapy; immunotherapy; cancer cell proliferation inhibitor; transforming growth factor-beta-antagonist; humanized antibody; chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized murine anti-TGF-beta antibody protein, chimL.chimH, SEQ: 28.
Monoclonal antibody; animal disease model; metastasis; cytostatic;
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31-MAR-2004; 2004US-0557951P.
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Synthetic.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-2005
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                                                                                                                                                                                                                                                                                                                                      Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy; autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin; CDR; complementarity determining region; VH; heavy chain variable region; VK; kappa chain variable region; mononuclear phagocyte; FCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-1), VH chains from human Igs NEWM or KDL, and VK chains from Ig REI. Sequences are provided for mouse 022 VH (AAR54931), humanized NEWH-based VH (022 NWVH, AAR54929), humanized KDL- based VH (022 KLVH, AAR54930), buring hab production, VH and VK CDNAs were PCR amplified using primers given in AAQ65378-87. Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was heteroantibody, bifunctional antibody and immunotoxin production.
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                                                                      1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanised antibodies to Fc receptors - used for diagnosis or for treatment of e.g. cancer, allergies and infectious and auto-immune
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                                                                                                              ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                              polymerase chain reaction; primer; site-directed mutagenesis; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511; DB 2; Length 112;
Pred. No. 2.2e-32;
6; Mismatches 7; Indels
                             Indels
Score 516; DB 9; L
Pred. No. 4.6e-32;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 23; 36pp; English
                                                                                                                                                                                                               AAR54933 standard; peptide; 112 AA
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 88.1%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US010384.
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                                                                                                                                                                                                                                                                     (revised)
(first entry)
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Best Local Similarity 88.3-
Port 98; Conservative
Query Match
Best Local Similarity 86.7
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDA-) MEDAREX INC.
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                                                                                                                                                                                                                                                                                                             MAb 022 VK chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1992;
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                                                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                  19-OCT-1994
                                                                                                                                                                                                                                         AAR54933;
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RESULT 7

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ADX37184

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cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
hepatocellular carcinoma; immunotherapy; light chain variable region;
SMS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an antibody that competitively inhibits the immunospecific binding of a human SMS-1 specific monoclonal antibody (huSMS-1) to a SMS-1 target antigen. The invention is useful in the fields of cancer biology and immunotherapy, in particular for diagnosing and treating mallignancies such as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is the mouse anti-SMS-1 antibody light chain variable (VL) region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody competitively inhibiting immunospecific binding of a human SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful in treating malignancies such as melanoma, breast cancer or hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse anti-SM5-1 antibody light chain variable region, SEQ ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 510; DB 9; Length 113;
Pred. No. 2.7e-32;
7; Mismatches 8; Indels
                                                                                                                                                                                                                     /note= "Variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYMB-) SYMBIGENE ACQUISITION CO INC.
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                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADV92466 standard; protein; 133 AA.
                                                                                                                                                                                                                                                                      95. .102
/note= "Variable
                                                                                                                                                                                                                                                      "Variable
                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-2004; 2004WO-US017855.
                                                                                                                                                                                                                                                                                                                                                                                                                          2003CN-00129123.
2003CN-01119926.
2003US-00722849.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 87.0%;
Local Similarity 86.6%;
Les 97; Conservative '
                   (first entry)
                                                                                                                                                                                                                                                          /note=
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N-PSDB; AEA88705.
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                                                                                                                                                                                                                                                                                                                        WO2005053604-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-2003;
26-NOV-2003;
                   25-AUG-2005
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                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                      Region
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to antibodies which are specific for the cancer associated antigen SM5-1. The antibodies are useful for assaying for SM5-1 antigen in a sample, which is useful for the prognosis or diagnosis of a neoplasm, e.g. melanoma, breast cancer, or heptcocallular carcinoma. The present sequence is a variable region of one such anti-SM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
2 IVWTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61
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                                                                                                                                                                                                                                                                                    Therapy; light chain variable region; SM5-1; neoplasm; tumor; hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFPSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
                                                                                                                                                                                                                                                     Murine SMS-1 antibody, mSMS-1, light chain variable region, SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that competitively inhibits the immunospecific binding chuman SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful for diagnosing or treating neoplasms, e.g. melanoma or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 510; DB 9;
Pred. No. 2.7e-32;
7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 4; 40pp; English.
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                                                                                                                                                  ADX37184 standard; protein; 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2003; 2003US-00722849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2003; 2003CN-00129123
25-NOV-2003; 2003CN-01119926
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                    Cytostatic; Gene
melanoma; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADX37188
                                                                                                                                                                                                                                                                                                                                                                         US2005031617-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GUOY/) MA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo Y;
                                                                                                                                                                                                                     21-APR-2005
                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-2005.
                                                                                                                                                                                     ADX37184;
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Best Local S
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AEA8870:

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Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
Novel chimeric protein-related mSM5-1 light chain protein SeqID10.
                                  protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 510; DB 9; Length 133;
86.6%; Pred. No. 3.1e-32;
iive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM5-1 chimeric antibody (ChSM) light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 10; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                            (SYMB-) SYMBIGENE ACQUISITION CO INC.
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                                                                                                                                                                                                                                                   , 2003CN-00129290.
; 2003CN-01119930.
2003US-00723003.
                                                                                                                                                                                                                     04-JUN-2004; 2004WO-US017765.
                                                                                                                                                                                                                                                                                                                 28-NOV-2003; 2003TW-00133577
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N-PSDB; ADV98528.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention.
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                                                                                                                                       WO2005001048-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Guo Y;
                                                                                                                                                                                                                                                                              :5-NOV-2003;
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                                                                                                                                                                                                                                                         13-JUN-2003;
                                                                                                                                                                                                                                                                                              26-NOV-2003;
                                                                                                                                                                              06-JAN-2005
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Chimeric.
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                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepstocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light chain variable region protein.
                                                                           Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                     /note= "Mature Mouse SMS-1 (mSMS-1) light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                         .133
.e= "Light chain variable region gene (VL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 133;
                                      Mouse SM5-1 (mSM5-1) light chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 510; DB 9; Le
86.6%; Pred. No. 3.1e-32;
iive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 10; 158pp; English
                                                                                                                                                                                                                                     "Signal peptide"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADV98529 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                         region protein"
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(first entry)
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Best Local Similarity 86.0.
Best Local 97; Conservative
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                                                                                                                                                                                                                                                                                                21. .133
                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2005-030218/03.
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N-PSDB; ADV92465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                              US2004254108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAJJ/) MA J. (GUOY/) GUO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2005
                                                                                                                                                           Mus musculus
  10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2004
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                                                                                                                                                                                                  Key
Peptide
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This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, such as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins of the invention. Note: Two sequences were allocated this SeqID number in the specification, the alternative sequence is shown on page 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYFSSYTFGGGTKLEIKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 510; DB 9; Length 239
86.6%; Pred. No. 5.3e-32;
___wiematches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .26
/label= Signal peptide
27. .661
                                                                                                                                                                                                                                        (SYMB-) SYMBIGENE ACQUISITION CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 9; 147pp; English.
                                                                                                                                                    25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
28-NOV-2003; 2003TW-00133577.
                                                                                              04-JUN-2004; 2004WO-US017765.
                                                                                                                                     13-JUN-2003; 2003CN-00129290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FL/Fc/chSMFv fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.6
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                     WPI; 2005-075540/08.
N-PSDB; ADV98532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 239 AA;
                  WO2005001048-A2.
                                                                                                                                                                                                                                                                               Ma J, Guo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-2005
                                                        06-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADV92490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              agent.
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%XCCCCCCCCXXX47474X88X548X8X6X6CCCCCCCCXX8X47474X88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl funoxicidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the SM5-1 chimeric antibody (ChSM)
                                                                                              'note= "Mature SMS-1 chimeric antibody (ChSM) light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFPSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 IMMIQSPSSLAVSAGEKVTMSCKSSQSVJ.YSSNQKNYLAWYQQKPGQSPKILIYWASTRE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel chimeric protein-related ChSM light chain protein SeqID14.
                                                                                                                                                      note= "Light chain variable region gene (VL) 34. .239
                                                                                                                                                                                                'note= "Human kappa chain constant cDNA (CL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510; DB 9; Length 239;
Pred. No. 5.3e-32;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 14; 158pp; English.
                                   .. .20
/label= Signal peptide
                cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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86.6%;
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25-NOV-2003; 2003CN-01119930.
                                                                                                                                                                                                                                                                                                                   26-NOV-2003; 2003US-00723003
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hes 97; Conservative
                                                                             21. .239
                                                                                                              protein"
                                                                                                                                     21. .133
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N-PSDB; ADV92469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 239 AA;
                                                                                                                                                                                                                                   US2004254108-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     (MAJJ/) MA J.
(GUOY/) GUO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guo Y;
                                                                                                                                                                                                                                                                           16-DEC-2004
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                           Protein
                                 Peptide
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protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
                                                                                                                                                             04-JUN-2004; 2004WO-US017765.
                                                                                                                                                                                       13-JUN-2003; 2003CN-00129290.
25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
28-NOV-2003; 2003TW-00133577.
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nes 97; Conservative
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N-PSDB; ADV98552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 661 AA;
                                                                                                     WO2005001048-A2
                                                                                                                                                                                                                                                                                            Guo Y;
                                             Homo sapiens
                                                                                                                                  06-JAN-2005
                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                            Ma J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the FL/Fc/chSMFv fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
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               27. .182
/note= "Flt3 ligand extracellular region (FLex)"
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                                                                                                                                                                             [VH)
                                                                                                                                                                                                                                     'note= "Light chain variable region gene (VL)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34.
"Mature FL/Fc/chSMFv fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 661;
                                                                                                                                                                             "Heavy chain variable region gene
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87.0%; Score 510; DB 9; L.
Best Local Similarity 86.6%; Pred. No. 1.3e-31;
Matches 97; Conservative 7; Mismatches 8;
                                                                                                                   'note= "Encoded by TGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; SEQ ID NO 34; 158pp; English
                                                                                                                                                                                                        "Linker region"
                                                           'note= "Hinge region"
                                                                                                                              .414
.e= "CH3 region"
                                                                       .98. .307
'note= "CH2 region"
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25-NOV-2003; 2003CN-01119930
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/note= "T.
557
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                                       .197
                                                                                                                                                             415. .5.
/note= '534. .59
                                                                                                                                                   /note=
   note=
                                                                                                                                  308.
                                            183.
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                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                  US2004254108-A1
                                                                                                                                                                                                                                                                                                                                                                                           (GUOY/) MA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Guo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
furuncle;
                                                                                                                                                                                           New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein; immunological; staphylococcal infection; impetigo; pneumonia; furuncle septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 510; DB 9; Length 66
Pred. No. 1.3e-31;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                           Claim 23; SEQ ID NO 34; 147pp; English.
(SYMB-) SYMBIGENE ACQUISITION CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE29266 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
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Region

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The invention relates to monoclonal antibody which binds the clumping factor A (ClfA) protein from Staphylococcus aureus. The anti-clfA monoclonal antibody is useful for treating or preventing S. aureus infection in a human or animal, and for inhibiting the binding of staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment S. aureus Clf40 protein, S. aureus Clf31 protein, or the S. aureus N3 protein is useful for inducing an immunological response in a human or animal. These staphylococcal infections include wound infections, sepsis, impetigo, furuncles, premenonia, septic archritis or endocarditis. The present sequence is Staphylococcus aureus ClfA specific monoclonal antibody 12-9VLA-1 (variable light sequence) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         New anti- clumping factor A (ClfA) monoclonal antibody, useful for treating or preventing Staphylococcus aureus infection e.g. wound infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in a human or animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.9%; Score 509; DB 5; Length 112; Best Local Similarity 87.4%; Pred. No. 3.2e-32; Matches 97; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                     Hall A;
                                                                                                                                                                                                                                                                                                                                                     Domanski P, Patel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 35; 80pp; English.
24. .40
/note= "CDR1"
                           56. .62
/note= "CDR2"
                                                                 95. .102
/note= "CDR3"
                                                                                                                                                                                                                          26-JAN-2001; 2001US-0264072P.
12-MR-2001; 2001US-0274611P.
18-JUN-2001; 2001US-039813P.
30-JUL-2001; 2001US-0308116P.
                                                                                                                                                                                         28-JAN-2002; 2002WO-US002296.
                                                                                                                                                                                                                                                                                                                                                    Patti JM, Hutchins JT,
                                                                                                                                                                                                                                                                                                                 (INHI-) INHIBITEX INC.
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-759834/82.
                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD46865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 112 AA;
                                                                                                                    WO200272600-A2
                                                                                                                                                      19-SEP-2002
                                  Region
                                                                   Region
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2 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112 62 셤 ð

2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61

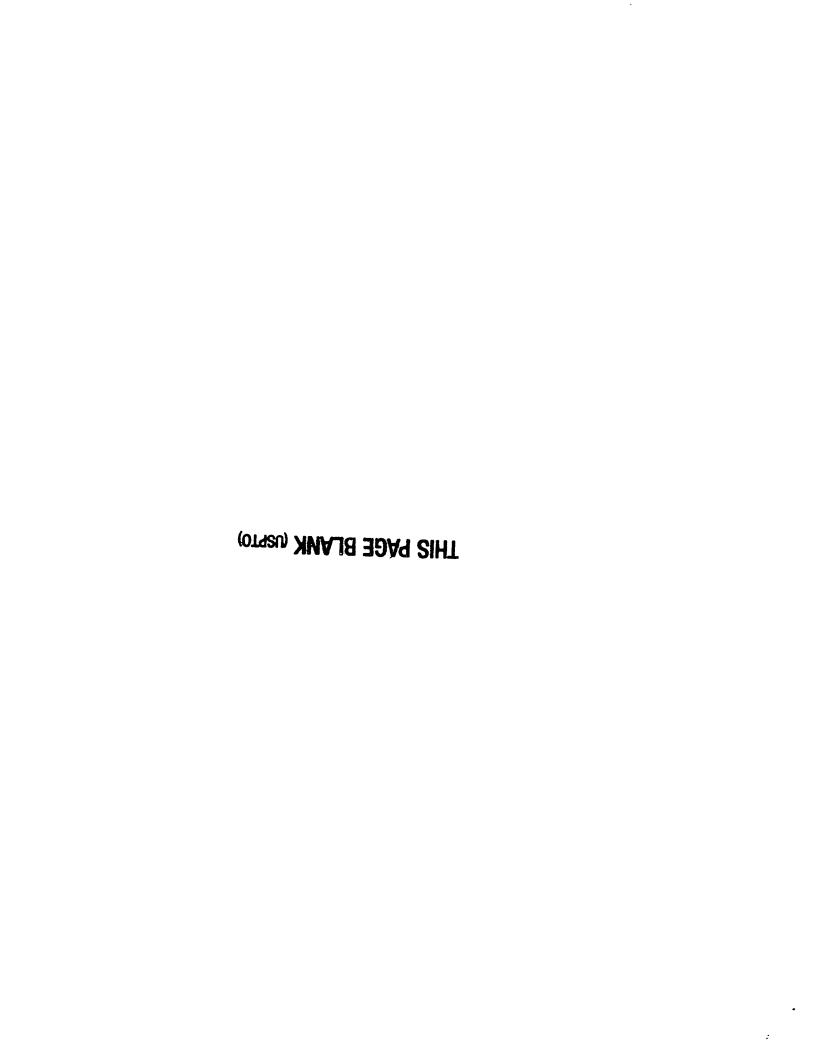
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Gaps

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Search completed: May 9, 2006, 01:25:26 Job time : 103.749 secs



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version 5.1.8 - 2006 Biocceleration Ltd.
GenCore (c) 1993
           Copyright
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- protein search, using sw model OM protein

Run on:

May 9, 2006, 01:25:51; Search time 17:1212 Seconds (without alignments) 635.031 Million cell updates/sec

US-10-700-632-10 586

1 EIVLTQSPGSLAVSPGERVT......CHQYLSSRTFGQGTKLEIKR 113 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

i.o.	chain V r	_		a chain pre	chain				chain		a chain pre		y light cha			chain	t chain V r						U	or monoclon		chain	chain	ı	chain
Description	kappa											kappa	tibody	kapp	light	kapp	light	ti-Sm	kappa	kappa	kapp	kappa	kappa	titumor	kappa	kappa	kappa	φ	light
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QI.		841393	PT0356	S26040	PH1054	S34002	809970	S43103	PS0023	K4HULN	PL0014	PL0265	S51147	S06084	PT0407	K4HUJI	S26337	849531	PC1214	A53261	830520	S34003	A31790	A49260	K4HU17	PL0263	S46373	JC2270	PT0408
B		7	~			~	~	7	~	-	7	7	~	~	~	-	7	7	~	7	7	~	~	~	П	7	7	7	7
Length	111	112	118	138	103	113	112	112	133	114	145	112	120	240	113	133	101	134	134	138	113	113	220	113	134	113	132	113	113
& Query Match	83.6	81.6	81.4	80.7	80.4	80.1	79.7	79.7	79.7	79.4	79.1	78.8	78.8	78.8	78.5		78.3	78.1	77.7	77.0	76.4	76.4	76.4	75.9	75.9	75.7	S.	75.5	75.4
Score	490	478	477	473	471	469.5	467	467	467	465.5	463.5	462	461.5	461.5	460	460	459	457.5	455.5	451	447.5	447.5	447.5	444.5	444.5	443.5	443.5	442.5	442
Result		7	m	4	C)	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain V r Ig light chain V-J To kanna chain (Ma	Ig light chain V r Ig light chain V r Ig light chain V r Ig kappa chain V r r kappa chain V r	19 kappa chain v 19 kappa chain V-1 19 kappa chain V-J 19 light chain V 17 to kappa chain V 17 kappa chain V 19	Ig light chain V r Ig kappa chain V-I Ig light chain V r anti-Sm antibody V Ig kappa chain V r
S30523 S38807 S68212	PH1102 PH1101 F30538	530538 S44116 PH1104	PH1050 G30601 PH1103 S49532 PL0264
000	10000	10000	00000
113	1011 4011 4011	1112	103 109 1129 113
74.5	4444	73.8	73.2
441.5	4335 4335 4335 55	4432 432 5.54 5.53 5.53 5.53	430 430 429 428 427.5
31	1 W W W W	, w w w 4	. 4. 4. 4. 4. 5. 11. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5.

## ALIGNMENTS

RESULT 1

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G30502

Ig kappa chain V region (A52) - mouse

Ig kappa chain V region (A52) - mouse

Ig kappa chain V region (A52) - mouse

C; Species Musiculus (house mouse)

C; Accession: G30502

R; Bilat, D.; Webster, D., Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A; Pitle: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m1

A; Reference number: A30502; MUD:88315787; PMID:2457627

A; Accession: G30502

A; Residuary

A; Residuals preliminary

A; Residuals: 1-111 < EIL.

A; Residuals: 1-111 < EIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP10000176AF0
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
```

Gaps ; 0 Query Match

83.6%; Score 490; DB 2; Length 111;
Best Local Similarity 84.5%; Pred. No. 7.5e-35;
Matches 93; Conservative 9; Mismatches 8; Indels

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SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEI 111 62 62 ò q

## RESULT 2

S41393

Ig kappa chain V region (12.5H VL) - mouse

Ig kappa chain V region (12.5H VL) - mouse

Ig kappa chain V region (12.5H VL) - mouse

C;Species Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001

C;Accession: S41393

R;Margaritte, C; Gilbert, D.; Brard, F.; Tron, F.

B;Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-D A;Reference number: S41393

A;Accession: S41393

A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-112 < MAR>
A; Cross-references: UNIPARC: UPI0000176CCB; EMBL: Z29536
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology < IMM>

81.6%; Score 478; DB 2; Length 112;

Query Match

F;41-121/Domain: immunoglobulin homology <IMM>

Similarity

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80.7%; Score 473; DB 2; 77.9%; Pred. No. 2.5e-33;
                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
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                                                                                                                                                         88; Conservative
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                                                                                                                      Best Local Similarity
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Best Local Si
Matches 89
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                                                                                          Query Match
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Ig Appa chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Musculus (house mouse)

R;Okamoto, M.; Honjo, T.

Nucleic Acids Res. 18, 1895, 1990

A;Reference number: S09216; MUID:90245589; PMID:2336368

A;Reference number: S09216; MUID:90245589; PMID:2336368

A;Residues: 1-138 <OKA>

A;Reference number: S78098

A;Accession: S78098

A;Accession: S78098

A;Residues: 1-87, W, 99-138 <OKW>

A;Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Mus musculus (house mouse)
Cispecies: Musr-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
Cidate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
Cidate: To recise to reci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Mus musculus (house mouse)
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
Accession: PT0356
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                                                                                                                                                                    1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR
                                                                                                                             1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                                                           Gaps
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F;26-138/Product: Ig kappa chain (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.4%; Score 477; DB 2; Length 118; Best Local Similarity 82.5%; Pred. No. 1e-33; Matches 94; Conservative 10; Mismatches 8; Indels
                                                           Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
Pred. No. 7.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (2B11.1) - mouse (fragment)
                 81.2%; Prec. ....
                                                           91; Conservative
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                           Best Local
Matches 9
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S26040
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Ig kappa chain V region - human

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 0.2-lec-1991 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: 534002; 530522

R;Mariette, X.; Tsapis, A.; Brouet, J.C.

Rimunol. 23, 846-851, 1993

A;Title: Nuclectidic sequence analysis of the variable domains of four human monoclonal

A;Reference number: 534001; MUID:93209281; PMID:7681398

A;Accession: S34002

A;Accession: S14002

A;Accession: S14002

A;Accession: S14002

A;Cross-references: UnTPARC:UPI0000176D32; EMBL:Z18328

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IVM>
P;16-96/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig light chain V region (clone 202.135) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1054
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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                                                                                                                                                               1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                                                                                                                                                                                                                                                                                           86 ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYFCQQYYSFLTFGAGTKLELKR 138
                                                                                                                                                                                                                                                       61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP10000176AAE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
S;Accession: 200023
R;Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A;fitle: Cloning and characterization of cDNAs coding for the heavy and light chains of A;Reference number: PS0023; MUID:89232725; PMID:3149944
A;Recession: PS0023
A;Rocession: Lyge: mRNA
A;Residues: 1-133 <a href="https://doi.org/10.10000176787">doi.org/10.10000176787</a>
                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain BALB/c

A, Note: the amino-terminal four residues of the mature protein were directly sequenced
C, Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aerug
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
C, Keywords: heterotetramer; immunoglobulin
F;1-20/omain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>
F;36-116/Domain: immunoglobulin homology <IMM>
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A,Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass
A,Reference number: A61458, WUID:90039128; PMID:2478651
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <!WM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a new kappa chain subgroup,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Accession: Appr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C;Accession: A01903; F61458
R;Schneider, M.; Hilschmann, N.
Hoppes-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe A;Reference number: A01903; MUID:76004342; PMID:50995
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A;Note: this is the first completely sequenced V region of a new kappa chain subgrous A;Note: the C region of this chain has the Inv (3) marker
A;Note: the C region of this chain has the Inv (3) marker
B;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 79.7%; Score 467; DB 2; Similarity 79.6%; Pred. No. 7.9e-33; 90; Conservative 11; Mismatches 12
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78.1%; Pred. No. 9.1e-33;
ive 13; Mismatches 11
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F;23-94/Disulfide bonds: #status predicted
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Best Local Similarity
Matches 90; Conserv
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Best Local S
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R; Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A; Reference number: S09955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-112 <REI>A;Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:g55406; PIDN:CAA36151.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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KGllbert, D.; Brard, F.; Margaritte, C.; Delpech, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
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A; Cross-references: UNIPARC:UP10000116626; EMBL; Z31353; NID:g467574; PIDN:CAAB3231.1;
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin c; Keywords: heterotetramer; immunoglobulin homology
F;16-96/Domain: immunoglobulin homology < IMM>
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                DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                       Ig kappa chain V-J region (4C8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-J region (4B1 VL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb_1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                                                                              61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112
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Best Local Similarity 77...
87; Conservative
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A, Accession: $43103
A, Status: preliminary
A, Molecule type: mRNA
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Matches 90; Conserv
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C;Accession: $51147
R;de Krulf, J.; Boel, E.; Logtenberg, T.
Ride Krulf, J.; Boel, E.; Logtenberg, T.
Submitted to the EMBL Data Library, January 1995
A;Description: Selection and application of human SCFV antibody fragments from a semi-sy A;Reference number: $51147
A;Accession: $51147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
Modecule type: mRNA
A;Residues: 1-120 - DEK>
A;Cross-references: UNIPARC:UP10000116210; EMBL:X83714; NID:g633227; PIDN:CAA58689.1; Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cjate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
CjAccession: 866084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
RvCleic Acids Res. 17, 7992, 1989
A;Title: Nuclectide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDN?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-240 <CRO>
A; Cross-references: UNIPARC: UP10000113764; EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PIF
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-240/Product: Ig kappa chain #status predicted <MAT>
F; 153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                   antibody light chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
                           21 DFVWTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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F;16-96/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.8%; Score 461.5; DB 2; Length : 78.1%; Pred. No. 2.1e-32; cive 12; Mismatches 12; Indels
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Best Local Similarity 78.1%;
Matches 89; Conservative 1:
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Best Local Similarity 78.18
Matches 89; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0265
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL023; MUID:9011618; PMID:2104919
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:9011618; PMID:2104919
A;Accession: PL0265
A;Molecule type: mRNA
A;Residues: 1-112 cSHL>
A;Cross-references: UNIPARC:UPI0000176AF3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroctetramer: immunoglobulin
F;123/Region: framework 1
F;12-26/Domain: immunoglobulin homology <IMM>F;24-40/Region: complementarity-determining 1
F;41-55/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residuces: 1-145 < CHE>
A, Cross references: WILPARC: UPI00001767A7
A, Residuces: 1-145 < CHE>
A, Cross references: WILPARC: UPI00001767A7
A, Experimental source: cell line F6-3
C, Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchc
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
C, Keywords: heterotetramer; immunoglobulin
C, Keywords: heterotetramer; immunoglobulin
C, F1-134/Product: Ig heavy chain V region (4C1) #status predicted < MAT>
F; 20/Domain: immunoglobulin homology < INM>
F; 44-60/Region: complementarity-determining 1
F; 76-82/Region: complementarity-determining 2
F; 115-123/Region: complementarity-determining 2
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                                                                                                                                                                                                 f kappa chain precursor V region (F6-3) - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DIVMSQSPSSLAVSVGEKVTMSCQSSQSLLYNSNQKNPLAWYQQKPQQSPKLLIYWASTR
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ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSS-RTFGQGTKLEIKR 113
                        61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYYSTPYSFGGGTKLEIKR 114
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F;135-145/Domain: constant region (fragment) #status predicted <COR>
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R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H Mol. Immunol. 25, 33-40, 1988
A,Fitele: Structural basis of Etimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424
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79.5%; Pred. No. 1.8e-32;
iive 10; Mismatches 13.
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F;63-94/Region: framework 3
F;95-102/Region: complementarity-determining 3
F;103-112/Region: framework 4
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Matches 89; Conservative
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Matches 89; Conservative
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RESULT 15 PT0407

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Filal light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30.5ep-1993 #text_change 21-Jan-2000
C;Date: 30.5ep-1993 #text_change 21-Jan-2000
C;Accession: PT0407
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Reference number: PT0376; MUID: 91147903; PMID: 1900082
A;Accession: PT0407
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homo sapien homo sapien

P01668 P06309 P04431 Q6pih7

Perfect score:

Sequence:

OM protein

Run on:

Minimum DB Maximum DB

Database

Searched:

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P01625;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-IV region Len.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salomon A.;
Submitted (AUG-1996) to Swiss-Prot.
-1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-1- MISCELLANEOUS: This is a Bence-Jones protein.
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R PDB; IEEG; X-ray; A/B=1-114.

R PDB; IEEG; X-ray; A/B=1-114.

R PDB; IEKG; X-ray; A-1-114.

R PDB; ILVB; X-ray; A-1-114.

R PDB; ILVB; X-ray; G=1-114.

R PDB; ILVB; X-ray; G=1-114.

R PDB; ALVB; X-ray; A-1-114.

R PDB; ALVB; X-ray; A-1-114.

R PDB; ALVB; X-ray; A-1-114.

R PDB; ELVB; X-ray; A-1-114.

R PDB; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray;

R PDB; X-ray; X-ray; X-ray; X-ray;

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R PDB; X-ray;

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MEDLINE=76004342; PubMed=50995;
Schneider M., Hilschmann N.;
"The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
KV1V HUMAN
GOULT 7 HUMAN
GOULT 9 HUMAN
GOULT 9 HUMAN
KV1A MÖUSE
KV3C HUMAN
GSBEÜF MOUSE
GEPITS HUMAN
KV1K HÜMAN
KV1K HÜMAN
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KV1W HUMAN
Q6PIH7 HUMAN
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-IV region JI precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Complementarity-determining-3.
Framework-4.
    Complementarity-determining-2.
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78.1%; Pred. No. 2.8e-40;
ive 13; Mismatches 11;
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MEDLINE=86041853; PubMed=2997712;
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Best Local Similarity 78.1%
Matches 89; Conservative
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HSSP; P01625; 1LVE.
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Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Ig kappa chain V-IV region JI. Framework-1. Complementarity-determining-1.
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Submitted (OCT-1986) to the BMBL/GenBank/DDBJ databases.
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10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-IV region B17 precursor.
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HSSP; P01625; 1LWB.
SMR; P06314; 21-134.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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01-APR-1988 (Rel. 07, Last seq
10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.0%
les 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             14633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE REVISION TO 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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P06314;
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Gaps

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REPAIR STANDARD C. Wallukat G., Tugler J., Maurice D., Roegel J.C.,

A Briand J.P., Hoebeke J.;

A Briand J.P., Hoebeke J.;

RI "Modulation of the M2 unscarinic acetylcholine receptor activity with

RT "Modulation of the M2 unscarinic acetylcholine receptor activity with

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RT "M4746180; CAG34081.1; -; Other_DNA.

DR RNSF; PRO837; IKCR.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGV; 2.

DR RNSFITE; PSS0835; IG_IKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSYNQKNYLAWYQQKPGQSPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                 1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 BSGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYC---HQYLSSRTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLS-SRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 74.0%; Score 433.5; DB 2; Length 255; 1 Similarity 76.5%; Pred. No. 1.2e-36; 88; Conservative 8; Mismatches 14; Indels 5;
                                                                                                                                                                                                                                                                                               DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                             Indels
   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 240 AA; 26609 MW; CP8630CCC002E52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 AA; 27445 MW; B68BD38395DF713B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                             Score 452.5; DB 2
Pred. No. 1.2e-38;
                                                                                                                                                                                                                                                                                                                               15; Mismatches
              EMBL; BC094049; AAH94049.1; -; mRNA.
SMR; Q52L64; 21-240.
InterPro; IPR003599; Ig.
InterPro; IPR003169; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR00306; Ig.
InterPro; IPR00396; Ig.
InterPro; IPR00396; Ig.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 1.
SMART; SM00406; IGY; 1.
PROSITE; PS50835; IG.LIKE; 2.
HUNCHPOSITE; PS50835; IG.LIKE; 2.
HUNCHPOSITE; PS50835; IG.LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ScFv B8E5 protein (Fragment).
Name=scFv B8E5;
                                                                                                                                                                                                                                                                                             77.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEKBOS MOUSE PRELIMINARY;
QEKBOS;
                                                                                                                                                                                                                                                                                                                               86; Conservative
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                                                                                                                                                                                                                                                                                                               Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                               1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                    21 DIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPPKLLIYWASTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLS-SRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                           78.1%; Score 457.5; DB 1; Length 134; 76.3%; Pred. No. 1.8e-39; ive 13; Mismatches 13; Indels 1.
                                                                                     kappa chain V-IV region B17.
                                                                                                                     Complementarity-determining-1.
                                                                                                                                                         Complementarity-determining-2.
                                                                                                                                                                                       Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                   Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                           134 AA; 14966 MW; 6413A22FD0738832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA.
                                                                                                                                                                                                                         By similarity.
                                                                                                                                                                           Framework-3.
                                                                                                                                           Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                 SMART; SM00406; IGv; 1.-
PROSITE; PS50835; IG LIKE; 1.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                             Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q52L64 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project;
                                                                                                                                                                                                                                                                                             Query Match
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                                                                       SIGNAL
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KV40 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
  197 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSY--PLTFGAGTKLEIK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQY-LSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DISBASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40/3 ....,
72.5%; Score 425; DB 1; Lengtn 12...
72.5%; Pred. No. 4.1e-36;
73.7%; Pred. No. 4.1e-36;
73.7%; Pred. No. 4.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [mmunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
RADPa chain V-III region HAH precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAS.
                                                                                                            129 AA
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SWR; P18135; 21-129.
Ensembl; ENGGO000169769; Homo sapiens.
GO; GO:0003825; C:extracellular region; NAC GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
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PROSITE; PS50835; IG LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.73
Matches 84; Conservative
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; PL0022; K3HUHA.
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129 AA;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukemia.
                                                                                                          KV3L HUMAN
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                                                              RESULT 6
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RESULT 7

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                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
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                                                                                                                                                                                                                                                                                             MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                              "Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-1.
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Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 420; DB 1; Length 12. Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                    single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
-!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-IV region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00406; IGv; 1.-
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13380 MW; 9586AD4188D33974 CRC64;
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10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-IV region precursor (Fragment)
Name=IGKV4-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000555; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z00023; CAA77318.1; -; Genomic_DNA.
PIR; A01902; K4HU.
HSSP; P01625; 1LVF.
SMR; P06312; 21-121.
Ensembl; ENSG0000153586; Homo sapiens.
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                                          Created)
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78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC; HGNC:5834; IGKV4-1.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            >121
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Best Local Similarity
                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                     01-JAN-1988
01-JAN-1988
10-MAY-2005
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P01623;
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KV3E_HUMAN
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                    Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840; Kipps T.J., Tomhave E., Chen P.P., Careon D.A.; "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."; J. Exp. Med. 167:840-852(1988).

-i. DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSS-RTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S6 ATGIPDRESGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPQTFGQSKVEIKR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                                                  GG: GO:0005576; C:extracellular region; NAS.
GG: GO:0005576; C:extracellular region; NAS.
GG: GO:0005955; P:amtigen binding; NAS.
GG: GO:0005955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SW00406; IG-v; Ig-v.
PROSITE; PS50835; IG-LIKE; I.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
BISULFID
BISULFID
BISULFID
BISULFID
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01-NOV-1990 (Rel. 16, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region HIC precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AA
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                                                                                                                                                                                                    PIR; A01892; K3HUSI.
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HSSP; P01625; 1EEQ.
                                                                                                                                                                                                                   HSSP; P01625; 1LVE.
SMR; P01620; 1-109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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P18136;
                                                                                                                                                                    removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                     Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                            MEDLINE=82046598; PubMed=6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE.
MEDLINE=82046598; PubMed=6794615;
Andrews D.W., Capra J.D.;
Andraw acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGv; 1.—
PROSTIR: PSES0835; IG_LIKB; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A01896; K3HUWL.
HSSP, P01625; 1LVE.
SMR; P01623; 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
21-JUL-1986 (Rel. 01, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) IG kappa chain V-III region WOL. Homo sapiens (Human).
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                                             PROTEIN SEQUENCE.
                                                                                                                        NCBI_TaxID=9606;
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9

Length 109;

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Local Similarity 69.34 nes 79; Conservative
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Q9UL78;
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PubMed=1552291;
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                                                                                                                                                                                                                                                                                        SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g kappa chain V-III region Ti.
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
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Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.6%; Score 414; DB 1; Length 129; Best Local Similarity 72.8%; Pred. No. 5.7e-35; Matches 83; Conservative 15; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                 PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14071 MW; 7395528EA2BB74D6 CRC64;
SMR; P18136; 21-129.
Ensembl; ENSG0000169769; Homo sapiens.
GO: GO:0005576; C:extracellular region; NAS.
GO: GO:0003823; F:antigen binding; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV;
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SMR, PO1622, 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
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129 AA;
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KV3D HUMAN
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv.
PR0STE; PS50815; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                    1 BIVLTQSPGTLSLSPGERATLSCRASQSV----SNSFLAWYQQKPGQAPRLLIYVASSR
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                                                                                                                                                                                                                                                  1 EIVLTOSPGSLAVSPGERVTMSCKSSOSVFFSSSOKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDILINE=98277139; PLDMed=9614934; DOI=10.1006/clin.1998.4531; MUX.Y. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
"Evidence for somatic selection of natural autoantibodies.";
J. Exp. Med. 175:983-991(1992).
EMBL; AF035036; AAD56272.1; -; mRNA.
                                                                                                                                                                             70.5%; Score 413; DB 1; Length 109; 69.3%; Pred. No. 6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                               11; Indels
                                                                                                                                             109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992)
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Clin. Immunol. Immunopathol. 87:184-192(1998)
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PIR; A30601; A30601.
PIR; A30608; A30608.
PIR; B30601; B30601.
PIR; B30601; B30601.
PIR; C30601; C30601.
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Gaps

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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altachul R. S., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Antachul S.F., Zeeberg B. Buetow K.H., Schemen C.M., Histeh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Makesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                              DB 1; Length 109;
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                                                                                     Complementarity-determining-1.
Framework-2.
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032451; AAH32451.1; -; mRNA.
                                                                                                                                                                                                                                                                          0C4F31EA11E12A0B CRC64;
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Last annotation update)
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                                   Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                             Score 406.5; DB 1
Pred. No. 2.8e-34;
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By similarity
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                                                                                                                                                                                                                                                                                                              69.48;
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE;
Direct protein sequencing;
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Les 77; Conservative
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                                                      mmunoglobulin V region.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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TISSUE=Abdominal adipose tissue;
TISSUE=Abdominal adipose tissue;
MEDLINE=98249779; PubMed=5588180; DOI=10.1006/bbrc.1998.8515;
Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: Rappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245:713-716(1998).
-I- FUNCTION: May play an important role in fibrillogenesis.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 Kappa chain V-IV region STH (Fragment).
Homo sapiens (Human).
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PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003596; Ig_v.
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InterPro; IPR003596; Ig_v.
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tes 83; Conservative
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PIR; S34096; S34096.
HSSP; P01625; 1EK3.
SMR; Q9UL78; 1-109.
                                                                    D30608.
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G30608.
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I30601.
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G30601;
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20-MAR-1987 (Rel. 04, Last sequence update)
20-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-III region GOL (Rheumatoid factor).
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE.
MEDILINE-86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
MEDILINE-86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
MEWAIR M., Chen P.B., Carson D.A., Posnett D., Capra J.D.;
"Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotypic group, in part predicted by its reactivity with antippeptide antibodies.";
MOI. Immunol. 23:239-244(1986).
                                                                                                                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSR--TFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                 DB 2; Length 236;
                                                                                                                                                                                                                                                                                                Indels
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PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
DISULFID 23 89 similarity.
                                                                                                                                                                                                                                                               Query Match 69.4%; Score 406.5; DB 2; Best Local Similarity 69.6%; Pred. No. 6.8e-34; Matches 80; Conservative 18; Mismatches 10;
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HSSP; P01625; LEK3.
SMR; P04206; 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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             SMR; Q6PILB; 21-236. InterPro; IPR003599; InterPro; IPR0031599; Ig. InterPro; IPR003597; Ig.cl. InterPro; IPR003006; Ig.MHC. InterPro; IPR003596; Ig. MHC. InterPro; IPR003596; Ig. V. Pfam; PP07654; Cl.set; I.
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
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109 AA;
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P04206;
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68.9%; Score 404; DB 1; Length 109; 67.5%; Pred. No. 5.1e-34; ive 19; Mismatches 12; Indels
                    77; Conservative
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 11, Appli
Sequence 115, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
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                                                                    May 9, 2006, 01:32:56 ; Search time 25.4372 Seconds (without alignments) 367.271 Million cell updates/sec
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Sequence
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                                                                                                                                    1 EIVLTQSPGSLAVSPGERVT......CHQYLSSRTFGQGTKLEIKR
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           GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/jaa/5_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6_COMB.pep:*
/cgn2_6/ptodata/1/jaa/H_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
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US-08-69-102A-2

US-09-155-107-2

US-10-125-107-2

US-10-146-305-17

US-09-419-788-115

US-09-419-788-115

US-09-419-788-115

US-09-419-788-115

US-09-127-902-6

US-09-127-902-6

US-09-127-902-6

US-09-127-902-6

US-09-125-107-6

PCT-US95-09641-6

US-09-125-114

US-09-125-114

US-09-125-114

US-09-128-114

US-09-128-116

US-09-128-116

US-09-16-116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-916-098A-56
US-08-428-257A-76
US-07-987-264-16
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                                                                                                                                                                                        572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                               US-10-700-632-10
586
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Match Length
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                                                                                                                                                          Scoring table:
                                                                                                                          Perfect score:
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475.5
475.5
471
471
467.5
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Maximum DB E
                                                  OM protein
                                                                                                                                     Sequence:
                                                                                                                                                                                         Searched:
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                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 511; DB 2; Length 112;
88.3%; Pred. No. 5.8e-41;
tive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ATTOIN BET B.
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: MXI-013
TELEPOMONICATION INFORMATION:
TELEPOMONICATION 1NFORMATION:
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-5941
TELECOMMUNICATION 1NFORMATION:
TELEPAX: (617) 227-5941
US-08-929-856-66
US-08-353-400-34
US-08-353-400-34
US-08-353-08435-6
US-09-490-105-17
US-09-490-15-17
US-09-490-15-17
US-09-160-567-11
US-09-160-567-11
US-09-100-509-031-11
US-08-828-741B-6
US-09-100-567-6
US-09-100-567-6
US-09-100-29-6
US-09-100-29-6
US-09-100-29-6
US-09-508-031-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMANIZED ANTIBODI
TITLE OF INVENTION: IMMUNOBLOBULIN G C
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPEMARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08435516; Patent No. 6500931; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.3
Matches 98, Conservative
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FRAGMENT TYPE: internal
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Sequence 2, Application US/09155107

Sequence 2, Application US/09155107

SEQUENCE 2, Application US/09155107

GENERAL INFORMATION:

APPLICANT: LEUNG, Shui-on

APPLICANT: LEUNG, Shui-on

APPLICANT: UN'S APPLICANT: US/09/1007

TITLE OF INVERNION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES

TITLE REPERENCE: 018733/0879

CURRENT PLILING DATE: 1998-11-17

CURRENT PLILING DATE: 1997-03-19

EARLIER PLILING DATE: 1997-03-19

EARLIER PLILING DATE: 1997-03-19

SOFTHARE: PLILING DATE: 1996-03-20

NUMBER OF SEQ ID NOS: 47

COURTHARE: PATENTING DATE: 1096-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIVLIQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.2%; Score 499; DB 2; Length 113;
85.8%; Pred. No. 7.9e-40;
tive 5; Mismatches 11; Indels
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
                                                                                                                                          FILING DATE:
CLASSIPFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-7UL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE BETHARD D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 18733/463/IMIN
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 113 amino acids
TYPE: amino acid
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Best Local Similarity 85.8
Matches 97; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Conservative
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US-09-155-107-2
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   Sequence 2, Application US/09127902
Patent No. 6187287
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOWA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
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85.2%; Score 499; DB 1; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels
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amino acid
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US-09-127-902-2
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Sequence 15, Application US/07916098A

Patent No. 5871732

GENERAL INPORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: TROMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, USEBPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMSÓSPSSLAVSVGEKVTMSCKSSÓSLLYSGNÓKNÝLAWYQQKPGÓSPELLIYWASTR 60
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          1 BIVLTOSPGSLAVSPGERVTMSCKSSOSVFFSSSOKNYLAWYQOIPGOSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SACK, Markus
APPLICANT: SACK, Markus
APPLICANT: SACK, Markus
APPLICANT: SACK, Markus
APPLICANT: MONECKE, Marchael
APPLICANT: MONECKE, Marchael
APPLICANT: MERRANA, Sabine
APPLICANT: SPIEGEL, Holger
APPLICANT: SPIEGEL, Holger
APPLICANT: SEMBERANS, Neil
TITLE OF INVENTION: Mestatance
TITLE OF INVENTION: Resistance
FILE REFERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
BARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                    ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYCQQYYSYRTFGGGTKLEIKR 113
                                                                                                                                                61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
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82.3%; Pred. No. 2.6e-38;
iive 10; Mismatches 10;
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ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115, Application US/09419788
Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 82.3$
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS;
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09641
FILING DATE: 11-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-AUG-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE: HANDELICATION
SEQUENCE: HANDELICATION
FOR SEQUENCE: HANDEL
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APPLICANT: YUHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
TITLE OF INVENTION: A S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REPERENCE: OV17440
CURRENT APPLICATION NUMBER: US/10/146,305
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR FILING DATE: 2001-05-16
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                                                                                                                                                ESGVPDRFTGSGSGTDFTLTISRVQVEDLAIYYCHQYLSSWTFGGGTKCLEIKR 113
                                                                                                        61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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83.4%; Score 489; DB 2; Length 130;
Best Local Similarity 82.3%; Pred. No. 8e-39;
Matches 93; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9509641 GENERAL INFORMATION:
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Patent No. 6939956
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amino acid
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Best Local Similarity 85.8
Matches 97; Conservative
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TYPE: PRT
ORGANISM: Escherichia coli
US-10-146-305-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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SOFTWARE: Kopatentin 1.71
SEQ ID NO 7
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TOPOLOGY:
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US-10-146-305-7
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REFERENCE/DOCKET NUMBER: MXI-013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08435516
Patent No. 6500931
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.8%; Score 485; DB 1; Length 112; Best Local Similarity 82.1%; Pred. No. 1.6e-38; Matches 92; Conservative 10; Mismatches 10; Indels
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CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: W 92 23377.4; PCT/US93/10384
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ATTOIG, BECH B.
REGISTRATION NUMBER: 35,430
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION NUMBER: PCT/US91/08843
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION NUMBER: 07/618,542
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFRENCEY/DOCKET NUMBER: 92,310-G
TELEPHONE: (312) 715-1000
TELEPHONE: (312) 715-1000
TELEPHONE: (312) 715-1234
TELEPHONE: (312) 715-1234
TELEPHONE: (312) 715-1234
TELEPHONE: CHARACTERISTICS:
LENGTH: 112 amino acids
TTYPE: amino acids
TTYPE: amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
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ILLINOIS
                          U.S.A.
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Sequence 6, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112
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                                                                                                                                                                                                                                                                                                Query Match 81.2%; Score 476; DB 2; Length 112; Best Local Similarity 78.6%; Pred. No. 1.1e-37; Matches 88; Conservative 14; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURKENI AFFLICATION DAIA:
PPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-UUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY AGENT INPORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/INTELECOMOVINICATION INFORMATION:
TELECHONE: (202)672-5399
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 110-201
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acids
TYPE: amino acid
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Best Local Similarity 78.8%
Matches 89; Conservative
                                                                                                                                                                                                   MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-690-102A-6
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US-08-690-102A-6
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
GENERAL INFORMATION:
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PCT-US95-09641-6
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Patent No. 6187287

GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOWA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                 9
                                    1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQLIQSPSSLSASVGDRVTMSCKSSQSVLYSANHKNYLAWYQQKPGKAPKLLIYWASTR 60
               BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                  ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRFGQGTKLEIKR 113
                                                                                                       ESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQYLSSWTFGGGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 2007-5109
COMPUTER REDABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAMME: SAXE, BETTHARD D.
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-155-107-6
; Sequence 6, Application US/09155107
; Patent No. 6254868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 amino acids
amino acid
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Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                US-09-127-902-6
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TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09641
FILING DATE: 11-AUG-1995
PRIOR APPLICATION NUMBER: US 08/289,576
FILING DATE: 11-AUG-1995
FILING DATE: 11-AUG-1995
FILING DATE: 11-AUG-1995
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids

"WUDE: AUG-1997
INFORMATION FOR SEQ ID NO: 6:
ESCUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
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APPLICANT: LEUNG, Shui-on
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: HANSEN, Hans
APPLICANT: QU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 01973/0879
CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1994-11-17
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATCHIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%; Score 476; DB 2; Length 113; 78.8%; Pred. No. 1.2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
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amino acid
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MOLECULE TYPE: protein
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Patent No. 6270765

GENERAL INFORMATION:

APPLICANT: Yashwart M. Deo

APPLICANT: Ocol Goldstein

APPLICANT: Cheziano

APPLICANT: Cheziano

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

VOMBERSPONDENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Yashwant M. Deo
APPLICANT: Robert Graziano
APPLICANT: Robert Sommanue
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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Matches 88; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: 
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US-08-661-052-14; Sequence 14, Application US/08661052; Patent No. 5837243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ATTOIG, BELL E.
REGISTRATION NUMBER: 35,430
REFRENCE/DOCKET NUMBER: MXI-CTELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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amino acid
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US-09-188-082-14
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1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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                           COMPUTED 1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                        APPLIAND DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 9, 2006, 01:35:39 Job time : 26.4372 secs
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.64
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
Massachusetts
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(without alignments)
556.303 Million cell updates/sec
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Sequence 28,
Sequence 4, A
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Sequence 10,
Sequence 10,
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Sequence 3
Sequence 3
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586
1 BIVLTQSPGSLAVSPGERVT......
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                                                                                        May 9, 2006, 01:57:07; Search time 84.8723 Seconds
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(gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-700-632-8
US-10-700-632-8
US-10-229-335-28
US-10-229-335-28
US-11-004-639-10
US-11-004-639-10
US-11-004-639-14
US-11-004-639-14
US-11-004-639-14
US-11-004-639-14
US-10-025-052-19
US-10-056-052-19
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US-11-089-190-14
                                                                                                                                                                                                                                                                        1867569 seqs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
             Copyright
                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                           Sequence:
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No.
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Sequence 10, Application US/10700632
Publication OF US20050118183A1
GENERAL INFORMATION:
TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA US/10/700,632
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT APPLICATION NUMBER: US 60/424,332
PRIOR APPLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 94
SOFUTANE: Patentin version 3.2
SEQ ID NO 10
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Publication No. US20050118183A1
GENERAL INFORMATION:
APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REFERENCE: A4427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT FILING DATE: 2003-11-05
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
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              US-11-088-777-14
US-11-088-569-14
US-11-088-693-14
US-11-089-368-14
US-11-089-368-14
US-11-013-537-2
US-10-146-305-7
US-10-146-305-7
US-10-830-899-56
US-10-830-899-56
US-10-831-62-56
US-10-861-662-63
US-10-861-662-63
US-10-229-335-4
US-10-229-335-4
US-01-229-335-4
US-01-239-358A-2
US-10-467-253-7
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ORGANISM: Artificial Sequence
US-10-700-632-10
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US-10-700-632-8
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Publication No. US20050031617A1
Publication No. US20050031617A1
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: ANTHODIES SPECIFIC FOR CANCER
TITLE OF INVENTION: ANTHODIES SPECIFIC FOR CANCER
FILE REFERENCE: 54906200010
CURRENT APPLICATION NUMBER: US/10/722,849
CURRENT PILING DATE: 2003-11-26
PRIOR FILING DATE: 2003-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.2%; Score 511; DB 4; Length 112;
88.3%; Pred. No. 1.5e-36;
iive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
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Pred. No. 1.8e-36;
                                                                                                                                                                                    MANE: ATTOOIG, BETH E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: 35,430

RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-7401

INFORMATION FOR SEQ ID NO: 28:
ENGINE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: applied

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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                                                                    CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
                      APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                           FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
86.6%;
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Matches 98; Conservative
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Best Local Similarity 86.6
Matches 97; Conservative
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TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
TITLE OF INVENTION: LEUKEMIA USING THE SAME
FILE REPERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700,632
CURRENT APPLICATION NUMBER: 2003-11-05
PRIOR PAPLICATION NUMBER: US 60/424,332
PRIOR FILING DATE: 2002-11-07
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Publication No. US20030144483A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
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                                                                                                                                                                       92.7%; Score 543; DB 5;
93.8%; Pred. No. 2.6e-39;
iive 3; Mismatches 4;
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Pred. No. 2.6e-39;
3; Mismatches 4.
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 62, Application US/10700632
Publication No. US20050118183A1
GENERAL INFORMATION:
     SOFTWARE: PatentIn version 3.2
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 93.8%;
Matches 105; Conservative
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                              Best Local Similarity 93.8 Matches 105; Conservative
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                                                                                                  ORGANISM: Mus musculus
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US-10-229-335-28
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LENGTH: 114
                                                                                                                         US-10-700-632-8
                           SEQ ID NO 8
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ORGANISM: Artificial Sequence
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SOFTWARE: Fablo
SEQ ID NO 10
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Sequence 47, Application US/11004659;
Publication No. US20050232926A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GUO, Yajun
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
TITLE OF INVENTION: ASSOCIATED ANTIGEN SM5-1 AND USES THEREOF
FILE REFERENCE: 54906200100
CURRENT FILING DATE: 2004-12-02
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US/10/722,849
PRIOR FILING DATE: 2003-11-26
PRIOR FILING DATE: 2003-11-26
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: INDOS: I
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Sequence 10, Application US/10723003

Publication No. US20040254108A1

GENERAL INFORMATION:

APPLICANT: MA, Jing

APPLICANT: MA, Jing

TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

FILE REFERENCE: 549062000200

CURRENT APPLICATION NUMBER: US/10/723,003

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: CN 2003101199300

PRIOR APPLICATION NUMBER: CN 201010199300

PRIOR PILING DATE: 2003-11-25

PRIOR PILING DATE: 2003-10-25

PRIOR PILING DATE: 2003-10-25

SOFTWARE PRIOR DATE: 2003-66-13

NUMBER OF SECULOR O
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Pred. No. 1.8e-36;
7; Mismatches 8
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87.0%; Score 510; DB 5;
Best Local Similarity 86.6%; Pred. No. 2.1e-36;
Matches 97; Conservative 7; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.0%;
Best Local Similarity 86.6%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Mus Musculus
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LENGTH: 133
TYPE: PRT
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LENGTH: 113
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Sequence 1.0 Application US/11004539
Publication On-1320550232911A1
Sequence 1.0 Application US/11004539
Publication No. US20550232911A1
SEQUENCE 1.0 Application US/10104539
PUBLICATION TOWNERS US/1000200
STILLS DESTRUCTION NUMBER: US/11/0004,639
CURRENT APPLICATION NUMBER: US/11/0004,639
STILLS DESTRUCTION NUMBER: US/11/0004,639
STILLS PRINCE PLING DATE: 2004-11-2
STILLS DATE: 2003-11-2
STILLS DATE: 2003-11-2
STILLS DATE: 2003-6-13
STILLS DATE: 2003-6-14
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RESULT 13
US-10-056-052-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                      82 SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYCHQYFSSYTFGGGTKLEIKR 133
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62 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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Sequence 34, Application US/10723003

Sequence 34, Application US/10723003

Publication No. US20040254108A1

GENERAL INFORMATION:

APPLICANT: MA, Jing

APPLICANT: MA, Jing

APPLICANT: GO, Yajun

TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

FILE REPERENCE: 549062000200

CURRENT APPLICATION UNMBER: US/10/723,003

CURRENT PILING DATE: 2003-11-25

FRIOR FILING DATE: 2003-11-25

FRIOR APPLICATION NUMBER: CN 031292909

FRIOR PILING DATE: 2003-06-13

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 661

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: PARTITUMEN BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/10/723,003
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-10-36
PRIOR FILING DATE: 2003-11-25
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87.0%; Score 510; DB 6;

Best Local Similarity 86.6%; Pred. No. 3.8e-36;

Matches 97; Conservative 7; Mismatches 8
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COTHER INFORMATION: Synthetic Construct
US-10-723-003-34
                                                                                                                                                                                                                                                         Sequence 14, Application US/11004639
Publication No. US:0050232931A1
GENERAL INFORMATION:
APPLICANT: MA, Jing
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US-11-004-639-14
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Length 661;

DB 5;

87.0%; Score 510;

Query Match

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                                                                                         2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61
                              Gaps
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Publication No. US2003009956A1

GENERAL INFORMATION:

APPLICANT: PATTI, Joseph M

APPLICANT: HUTCHINS, Jeff T

APPLICANT: HOTCHINS, Jeff T

APPLICANT: HALL, Andrea

APPLICANT: HALL, Andrea

TITLE OF INVENTION: MONOCLOMAL ANTIBODIES TO THE CLFA PROTEIN . . . .

FILE REFERENCE: PO1059408AS

CURRENT FILING DATE: 2002-04-19

PRIOR PLILORIS JOHNSER: 60/208,116

PRIOR PAPLICATION NUMBER: 60/208,413

PRIOR PAPLICATION NUMBER: 60/208,413

PRIOR PPLING DATE: 2001-06-18

PRIOR PPLING DATE: 2001-06-18

PRIOR PPLING DATE: 2001-06-18

PRIOR PLING DATE: 2001-06-18

PRIOR PLING DATE: 2001-06-18

PRIOR PLING DATE: 2001-06-18

PRIOR PLING DATE: 2001-06-18
                                                                                                                                                                                                           62 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT FILING DATE: 2004-11-202
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR APPLICATION NUMBER: CN 201010199300
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR PILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR PILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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Best Local Similarity 86.6%; Pred. No. 1e-35; Matches 97; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Construct US-11-004-639-34
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/11004639
Publication No. US20050232931A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61
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Sequence 6, Application US/10056052
Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: HOMANSKI, Paul
APPLICANT: HALL, Andrea
APPLICANT: HALL, Andrea
CURRENT HALL, Andrea
PRIERERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: 60/308,116
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR APPLICATION NUMBER: 60/298,413
                                                                                                                                                                                                                                                                                                                                                                                                                                          62 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLBIK 112
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Publication No. US20040229301A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Tissue Factor Antibodies and Uses Thereof FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                           Query Match 86.9%; Score 509; DB 4; Length 112; Best Local Similarity 87.4%; Pred. No. 2.2e-36; Matches 97; Conservative 7; Mismatches 7; Indels
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PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SRQ ID NO 10
LENGTH: 112
                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus
US-10-056-052-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-31
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US-10-816-938-31
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Sequence 33, A Sequence 70, A Sequence 17, A Sequence 27, A

Sequence 27, Appl Sequence 71, Appl Sequence 71, Appl Sequence 91, Appl Sequence 91, Appl Sequence 31, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 37, Appl Sequence 71, Appl Sequence 71, Appl Sequence 71, Appl Sequence 72, Appl Sequence 73, Appl Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl Sequence 77, Appl Sequence 71, Appl Sequence 71,

Sequence 5, 1 Sequence 26, Sequence

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OM protein

Run on:

Minimum DB Maximum DB

Database

Searched:

Sequence:

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Sequence 1, Application US/10981356A
; Bublication NO. US20060015952A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR PILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 1
; LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR
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86.7%; Pred. No. 8.2e-31;
ive 8; Mismatches 7; Indels
                                                                                                US-11-219-563-91

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US-10-814-397-31

US-10-834-397-49

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US-10-981-356A-30

US-11-096-046-30

US-11-056-046-30

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nes 98; Conservative
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ORGANISM: Mus musculus
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Sequence 29, Appl
Sequence 10, Appl
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Sequence 22, Appl
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Sequence 28, 1
Sequence 26, Al
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1 EIVLTQSPGSLAVSPGERVT......CHQYLSSRTFGQGTKLEIKR
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US-11-096-046-25

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Maximum Match 100%
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Result ě

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APPLICANT: TEJADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
FILE REFERENCE: P1954R1US
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 29
                                                                                                                                                                                                   LENGTH: 667
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Sequence 29, Application US/10981356A

Publication No. US20060015952A1

GENERAL INFORMATION:
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT:
TITLE OF INVENTION NUMBER: US/10/981,356A

CURRENT PILING DATE: 2004-11-04

PRIOR PELLING DATE: 2004-11-13

PRIOR PELLING DATE: 2004-11-13

PRIOR PELLING DATE: 2004-11-13

PRIOR PILING DATE: 2004-03-31

PRIOR PILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 45

LENGTH: 666
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APPLICANT: TEJADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGP-Beta Antibodies
FILE REFERENCE: P1954R1US
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                           Score 516; DB 11; 1 Pred. No. 8.2e-31; 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.1%; Score 516; DB 9; Lv
86.7%; Pred. No. 3.1e-30;
tive 8; Mismatches 7;
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                                                                                                                                                                                                                                                                                                              88.1%;
86.7%;
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Best Local Similarity 86.74
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 86.7
Matches 98; Conservative
                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                     LENGTH: 116
                                                                                                                                                                                                                                                                     US-11-096-046-1
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                                                                                                                                                                              SEQ ID NO 1
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                                                                                                                                                                                                                                         1 BIVLTQSPGSLAVSPGERVTMSCKSSQSVPFSSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
                                                                                                                                                                                                                                                               1 DIMMIQSPSSLAVSAGEKVIMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
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                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                             61 ESGVPDRPTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                               61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYCHQYLSSDTFGGGTKLEIKR 113
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                                                                                                                                                                        Length 667;
                                                                                                                                                                                                           Indels
                                                                                                                                                                       Query Match 88.1%; Score 516; DB 11; Best Local Similarity 86.7%; Pred. No. 3.1e-30; Matches 98; Conservative 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                    OTHER INFORMATION: sequence is synthesized
                                                                                                 LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/11136559
Publication No. US20050287164A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: POWANSKI, Paul
APPLICANT: PATEL, Paul
APPLICANT: HATLA, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus aureus
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97; Conservative
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Best Local Similarity
                                                                                      NAME/KEY: Unsure
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US-11-136-559-10
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                                                                       FEATURE:
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Sequence 29, Application US/11096046
Publication No. US20050276802A1
GENERAL INPORMATION:
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: FILVARORY, ELLEN H.
APPLICANT: MAO, WEIGUANG
APPLICANT: PRESTA, LEONARD G.

US-11-096-046-29

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1 DIVMTQSPDSLAVSLGERVTMNCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
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APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REPERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-03-12
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                                                                                                                                                                                                                                                                         Score 507; DB 11;
Pred. No. 3.5e-30;
8; Mismatches 7;
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86.5%; Pred. No. 6.8e-30;
tive 7; Mismatches 8;
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                                                                                                                                                                                     ORGANISM: Staphylococcus aureus
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   PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.6%;
Matches 97; Conservative
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Best Local Similarity 86.55
Matches 96; Conservative
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                                                                                                                      LENGTH:
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APPLICANT: PATTI, JOSEPH M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOWANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
APPLICANT: HALL, Andrea
TITLE OF INVERTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REPERENCE: PO7069USQ4/BaS
CURRENT FILING DATE: 2005-05-25
RICH APPLICATION NUMBER: US/11/136,559
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
   SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112
                                                     SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                  GARBARAL INCREMITY, JOSEPH M
APPLICANT: PATTI, JOSEPH M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOWNSKI, Paul
APPLICANT: DOWNSKI, Paul
APPLICANT: HALL, Andrea
ITITE OF INVENTYON: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REPRENCE: PO706990504/Bas
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT APPLICATION NUMBER: US/10/056,052
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-03-12
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Publication No. US20050287164A1
GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 6, Application US/11136559
Publication No. US20050287164A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKGANISM: Staphylococcus aureus
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GENERAL INFORMATION.

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: resistance against fungi

FILE REFERENCE: 3581.01US01

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
       198 ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPFTFGSGTKLEIKR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
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Best Local Similarity 82.5%; Pred. No. 5.4e-28;
Matches 94; Conservative 9; Mismatches 10
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                                                                                                                               ; Sequence 68, Application US/10512184; Publication No. US20050244901A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                       US-10-512-184-68
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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 | IMMTQSPSSLAVSAGEKVTWSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IVLIQSPGSLAVSPGERVTMSCKSSQSVPFSSSQKNYLAWYQQIPGQSPRLLIYWASTRE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: scFv VDcw with OTHER INFORMATION: specificity against Verticillium dahliae; OTHER INFORMATION: originates from Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFTGSGSGTDFTLTISSVQAEDLAVYCCHOYLSSYTFGGGTELEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112
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                                                                                             TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN. FILE REFERENCE: P07069US04/BAS CURRENT APPLICATION NUMBER: US/11/136,559 CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 496; DB 11;
Pred. No. 2.2e-29;
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Best Local Similarity 82.5%; Pred. No. 4.5e-28;
Matches 94; Conservative 9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                PRIOR PAPLICATION NUMBER: US/10/056,052
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTING VERSION 3.1
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/10512184
Publication No. US20050244901A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
HUTCHINS, Jeff T
DOMANSKI, Paul
PATEL, Pratiksha
HALL, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.6%;
Matches 95; Conservative
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LENGTH: 259
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APPLICANT:
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                                                                                                                                                              Sequence 3, Application US/10981356A; Sequence 3, Application US/10981356A; Publication No. US20060015952A1; GENERAL INFORMATION:

APPLICANT: FILVAROFF, ELLEN H.

TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT; FILE REFERENCE: P2068R1

CURRENT APPLICATION NUMBER: US/10/981,356A; CURRENT FILING DATE: 2004-11-03; PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 3
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ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLS-SRTFGQGTKLEIKR 113
                          ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPPTFGSGTKLEIKR 321
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## Sequence 27, Application US/10981356A

## Sequence 27, Application US/10981356A

## Publication No. 220060015952A1

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61 ESGVPDRFTGSGSGTDFTLTISSVQPEDLAIYYCHQYLSSRTFGQGTKLEIKR 113
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81.2%; Score 476; DB 9; Length 666;
Best Local Similarity 77.0%; Pred. No. 2.3e-27;
Matches 87; Conservative 16; Mismatches 10; Indels
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TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT FILLE REFERENCE: P2068H1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398
PRIOR PILING DATE: 2003-11-13
PRIOR PILING DATE: 2003-11-13
PRIOR PILING DATE: 2004-03-31
PRIOR FILING DATE: 2004-03-31
PRIOR FILING DATE: 2004-03-31
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                                                                                                                                                                                                                                                          APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: FILVAROPE, ELLEN H.
APPLICANT: MAO, WEIGUANG
APPLICANT: PRESTA, LEONARD G.
APPLICANT: TEJADA, MAX L.
TITLE OP INVENTION: Humanized Anti-TGF-Beta Antibodies
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CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
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                                                                                                                                            Sequence 3, Application US/11096046 Publication No. US20050276802A1 GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Matches 87; Conservative
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Matches 87; Conservative
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US-10-981-356A-25
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